

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 08:47:48 ; Search time 1 Seconds
(without alignments)
5.870 Million cell updates/sec

Title: us-09-402-569-4

Perfect score: 1443

Sequence: 1 agtctgctgaagtcaccca.....ttatctctctctctacacataa 1443

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 2034 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : us-09-009-893a-1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1441.4	99.9	2034	1 us-09-009-893a-1	
2	25.2	1.7	2034	1 us-09-009-893a-1	

ALIGNMENTS

RESULT 1
us-09-009-893a-1

Query Match 99.9%; Score 1441.4; DB 1; Length 2034;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGCTGCTGAGTCAATCATCAGGTGAAGAGCACTTGATACAGATCAGAGGAGATG 60
Db	268	ATGCTGCTGAGTCAATCATCAGGTGAAGAGCACTTGATACAGATCAGAGGAGATG 327
Qy	61	CTGCTCTTTTGTGCGGGATGTTGCTATAGATGTGTTCCACTTAATGTCAAGGACCTT 120
Db	328	CTGCTCTTTTGTGCGGGATGTTGCTATAGATGTGTTCCACTTAATGTCAAGGACCTT 387
Qy	121	CTGGATATTTTACGGAAAGAGTAAAGTGTCTGTGTCGGGACTTGCTGAACCTGTCTAC 180
Db	388	CTGGATATTTTACGGAAAGAGTAAAGTGTCTGTGTCGGGACTTGCTGAACCTGTCTAC 447
Qy	181	AGAGTGAAGGGATTTACCTGCTCAACGTAATCTTGAAGATGACAGAAAGCTGTGGAG 240
Db	448	AGAGTGAAGGGATTTACCTGCTCAACGTAATCTTGAAGATGACAGAAAGCTGTGGAG 507
Qy	241	ACCCACTGTCTAGGAACCTCACCTTGTGTTGGACTATAGAGTGTGATGCGAGAGATT 300
Db	508	ACCCACTGTCTAGGAACCTCACCTTGTGTTGGACTATAGAGTGTGATGCGAGAGATT 567

Qy	301	GGTGAGGATTTGGATAAAATCTGATGTCTCTCATTAATTTTCTCTCATGAAGATTACATG 360
Db	568	GGTGAGGATTTGGATAAAATCTGATGTCTCTCATTAATTTTCTCTCATGAAGATTACATG 627
Qy	361	GGCCGAGGCAAGATAAGCAAGGAGAGAGTTTCTTGGACCTTGTGTTGAGTTGAGAA 420
Db	628	GGCCGAGGCAAGATAAGCAAGGAGAGAGTTTCTTGGACCTTGTGTTGAGTTGAGAA 587
Qy	421	CTAAATCTGGTTGCCCCCAGATCAACTGGATTATTATAGAAAAATGCTTAAAGAACATCCAC 480
Db	688	CTAAATCTGGTTGCCCCCAGATCAACTGGATTATTATAGAAAAATGCTTAAAGAACATCCAC 747
Qy	481	AGAATAGAGCTGAAGCAAAAAATCCAGAAAGTACAGAGCAGTCTGTTCAAGGAGCAGGAGCA 540
Db	748	AGAATAGAGCTGAAGCAAAAAATCCAGAAAGTACAGAGCAGTCTGTTCAAGGAGCAGGAGCA 807
Qy	541	AGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCTTCAAAATAAC 600
Db	808	AGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCTTCAAAATAAC 867
Qy	601	TTCAGGCTCCATAATGGGAGAAAGTAAAGAACAAAGACTTTAAGGAAACAGCTTGGCGCTCAA 660
Db	868	TTCAGGCTCCATAATGGGAGAAAGTAAAGAACAAAGACTTTAAGGAAACAGCTTGGCGCTCAA 927
Qy	661	CAAGAACCAAGTGAAGAAATCCATTCAAGGAATCAGAAAGCTTTTGGCTCAGAGCATACCT 720
Db	928	CAAGAACCAAGTGAAGAAATCCATTCAAGGAATCAGAAAGCTTTTGGCTCAGAGCATACCT 987
Qy	721	GAAGAGAGATCAAGATGAAGAGCAAGCCCTTAGGAATCTGCTCTGATATCATGTCATT 780
Db	988	GAAGAGAGATCAAGATGAAGAGCAAGCCCTTAGGAATCTGCTCTGATATCATGTCATT 1047
Qy	781	GGCAATGAGACAGAGCTTCTTCAGAGACACTTCACTTCCCTGGGCTATGAAGTCCAGAAA 840
Db	1048	GGCAATGAGACAGAGCTTCTTCAGAGACACTTCACTTCCCTGGGCTATGAAGTCCAGAAA 1107
Qy	841	TTCTTTCATCTCAGTATGATGGTATATCCAGATTTCTTGGCCAAATTTGCTGTATGCC 900
Db	1108	TTCTTTCATCTCAGTATGATGGTATATCCAGATTTCTTGGCCAAATTTGCTGTATGCC 1167
Qy	901	GAGCACCGAGACTACGACAGCTTTCTGTGTGTGTCCTGTGAGCGGAGGAGGCTCCCAAGCT 960
Db	1168	GAGCACCGAGACTACGACAGCTTTCTGTGTGTGTCCTGTGAGCGGAGGAGGCTCCCAAGCT 1227
Qy	961	GTGTATGTGTGGATCAGACTCACTCAGGGCTCCCTCTGCATCAGATCAGGAGGATGTT 1020
Db	1228	GTGTATGTGTGGATCAGACTCACTCAGGGCTCCCTCTGCATCAGATCAGGAGGATGTT 1287
Qy	1021	ATGGAGATTTCAATGCCCTTTATCTAGAGGAAAGCCAAAGATGTTTTTTTATTCAGAACTAT 1080
Db	1288	ATGGAGATTTCAATGCCCTTTATCTAGAGGAAAGCCAAAGATGTTTTTTTATTCAGAACTAT 1347
Qy	1081	GTGGTGTGAGGGCCAGCTGGAGGACAGCGCTTCTTGGAGGTGATGGGCCAGCGATG 1140
Db	1348	GTGGTGTGAGGGCCAGCTGGAGGACAGCGCTTCTTGGAGGTGATGGGCCAGCGATG 1407
Qy	1141	AAAGATGTGGAATTCAGGGCTCAGAAAGGAGGAGGCTGTGCACAGTTTCCCGAAGCTGAC 1200
Db	1408	AAAGATGTGGAATTCAGGGCTCAGAAAGGAGGAGGCTGTGCACAGTTTCCCGAAGCTGAC 1467
Qy	1201	TTCTTCTGAGGCTGTGTACTGCGGACATGTCCCTGCTGGAGCAGTCTCAGAGCTCACCA 1260
Db	1468	TTCTTCTGAGGCTGTGTACTGCGGACATGTCCCTGCTGGAGCAGTCTCAGAGCTCACCG 1527
Qy	1261	TCCTGTACTGAGGCTGTCTCCAGAAACTGAGCAAGAAAGAAAGCGCCACTCTCTG 1320
Db	1528	TCCTGTACTGAGGCTGTCTCCAGAAACTGAGCAAGAAAGAAAGCGCCACTCTCTG 1587
Qy	1321	GATCTTTCATTTGAATCAATGGCTACATGTATGATTTGAAACAGCAGAGATTCTTCTGCCAAG 1380
Db	1588	GATCTTTCATTTGAATCAATGGCTACATGTATGATTTGAAACAGCAGAGATTCTTCTGCCAAG 1647

Qy	1381	GAGAAATATTATCTCTGGCTGCAGCACACTCTGAGAAAGAAACTTATCCTCTCCTACACA	1440
Db	1648	GAGAAATATTATCTCTGGCTGCAGCACACTCTGAGAAAGAAACTTATCCTCTCCTACACA	1707
Qy	1441	TTAA	1443
Db	1708	TTAA	1710

RESULT 2
us-09-009-893a-1/c

Query Match	1.7%	Score 25.2;	DB 1;	Length 2034;
Best Local Similarity	66.7%	Pred. No. 0;		
Matches 36;	Conservative 0;	Mismatches 18;	Indels 0;	Gaps 0;

Qy	945	AGGAGGCTCCAGAGTGTATGGTGGATCAGACTCAGGCTCCCT	998
Db	1265	AGGGGAGCCCTGAGTGAGTGTATCCACACACTCTGGAGCCTCT	1212

Search completed: September 30, 2005, 08:47:50
Job time : 2 secs

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OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 08:46:37 ; Search time 1 Seconds
(without alignments)
5.902 Million cell updates/sec

Title: us-09-402-569-4
Perfect score: 1443
Sequence: 1 agtctgctgaagtcatcca.....ttatctctctctacacataa 1443

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 2045 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : us-08-795-088a-1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1441.4	99.9	2045	1	us-08-795-088a-1
2	25.2	1.7	2045	1	us-08-795-088a-1

ALIGNMENTS

RESULT 1
us-08-795-088a-1

Query Match 99.9%; Score 1441.4; DB 1; Length 2045;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATGCTGCTGAAGTCATCCATCAGGTGTAAGAAGCACTTGATACAGATGGAAGGAGATG	60
DB	511	ATGCTGCTGAAGTCATCCATCAGGTGTAAGAAGCACTTGATACAGATGGAAGGAGATG	570
QY	61	CTGCTCTTTTGTGCGGGATGTTGCTATAGATGTGTTCCACCTAATGTCAGGGACCTT	120
DB	571	CTGCTCTTTTGTGCGGGATGTTGCTATAGATGTGTTCCACCTAATGTCAGGGACCTT	630
QY	121	CTGGATATTTTACGGAAAGAGGTAAGCTGCTGTGTCGGGACTTGGCTGAACCTGCTAC	180
DB	631	CTGGATATTTTACGGAAAGAGGTAAGCTGCTGTGTCGGGACTTGGCTGAACCTGCTAC	690
QY	181	AGAGTAGGGCGATTGACCTGCTCAACCGTATCTTGAAGATGACAGAAAAGCTGTGGAG	240
DB	691	AGAGTAGGGCGATTGACCTGCTCAACCGTATCTTGAAGATGACAGAAAAGCTGTGGAG	750
QY	241	ACCCACCTGCTCAGGACCTCCTGTTTTCGGACTATAGATGTGTTGCGCAGAGATT	300
DB	751	ACCCACCTGCTCAGGACCTCCTGTTTTCGGACTATAGATGTGTTGCGCAGAGATT	810

QY	301	GGTGAGGATTTGGATTAATCTGATGTGCTCTCATTAATTTTCTCATGAAGGATTAATG	360
DB	811	GGTGAGGATTTGGATTAATCTGATGTGCTCTCATTAATTTTCTCATGAAGGATTAATG	870
QY	361	GGCCGAGGCAAGATTAAGCAAGGAGAGAGTTCCTTGACCTTGCTGAGTTGGAGAA	420
DB	871	GGCCGAGGCAAGATTAAGCAAGGAGAGAGTTCCTTGACCTTGCTGAGTTGGAGAA	930
QY	421	CTAAATCTCGTTGCCCCAGATCAATCGGATTTATTAAGAAAATGCTTAAGAAACATCCAC	480
DB	931	CTAAATCTCGTTGCCCCAGATCAATCGGATTTATTAAGAAAATGCTTAAGAAACATCCAC	990
QY	481	AGATATAGACTGAAGNCAAAATCCAGAGTACAGCAGTCTGTTTCAAGGAGCAGGACA	540
DB	991	AGATATAGACTGAAGNCAAAATCCAGAGTACAGCAGTCTGTTTCAAGGAGCAGGACA	1050
QY	541	AGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCTTCAATAAC	600
DB	1051	AGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGATCTTCAATAAC	1110
QY	601	TTCAGGCTCCATAATGGGAGAGTAAAGAACAAAGACTTTAAGGAAACAGCTTGGCGTCAA	660
DB	1111	TTCAGGCTCCATAATGGGAGAGTAAAGAACAAAGACTTTAAGGAAACAGCTTGGCGTCAA	1170
QY	661	CAAGAACCAGTGAAGNAAATCCATTCAGGAATCAGAACTTTTGTGCTCAGAGCATACT	720
DB	1171	CAAGAACCAGTGAAGNAAATCCATTCAGGAATCAGAACTTTTGTGCTCAGAGCATACT	1230
QY	721	GAAGAGAGATACAAGATGAAGCAAGCCCTTAGGAATCTGCTGATAATTCGATTCGATT	780
DB	1231	GAAGAGAGATACAAGATGAAGCAAGCCCTTAGGAATCTGCTGATAATTCGATTCGATT	1290
QY	781	GGCAATGAGACAGAGCTTCTTCGAGACACCTTTCACCTCCCTGGGCTATGAAGTCCAGAA	840
DB	1291	GGCAATGAGACAGAGCTTCTTCGAGACACCTTTCACCTCCCTGGGCTATGAAGTCCAGAA	1350
QY	841	TTCTTGATCTCAGTATGATGATATATCCAGATTCCTTGGCCAAATTTGCTGTATGCC	900
DB	1351	TTCTTGATCTCAGTATGATGATATATCCAGATTCCTTGGCCAAATTTGCTGTATGCC	1410
QY	901	GAGCACCAGACTTAGCAGACGCTTTGTGTGCTGCTGAGCGGAGGAGGCTCCAGAGT	960
DB	1411	GAGCACCAGACTTAGCAGACGCTTTGTGTGCTGCTGAGCGGAGGAGGCTCCAGAGT	1470
QY	961	GTGTATGTTGGATCAGACTCACTCAGGGCTCCCCCTGCATCACATCAGGAGGATGTC	1020
DB	1471	GTGTATGTTGGATCAGACTCACTCAGGGCTCCCCCTGCATCACATCAGGAGGATGTC	1530
QY	1021	ATGGGAGATTCATGCCCTTATCTAGCAGGAAGCCAAAGATGTTTTTATTCAGAACTAT	1080
DB	1531	ATGGGAGATTCATGCCCTTATCTAGCAGGAAGCCAAAGATGTTTTTATTCAGAACTAT	1590
QY	1081	GTGGTGTAGAGGGCCAGCTGGAGGACAGCAGCTCTTGGAGGTGATGGCCAGCGATG	1140
DB	1591	GTGGTGTAGAGGGCCAGCTGGAGGACAGCAGCTCTTGGAGGTGATGGCCAGCGATG	1650
QY	1141	AAGATGTGGAATTTCAAGGCTCAGAGCGAGGGCTGTGCACAGTTTCCCGAGAAGCTGAC	1200
DB	1651	AAGATGTGGAATTTCAAGGCTCAGAGCGAGGGCTGTGCACAGTTTCCCGAGAAGCTGAC	1710
QY	1201	TTCTTCTGAGGCTGTGTAATCTCGGACATGTCCTGCTGGAGCAGTCTCAGAGTCACCA	1260
DB	1711	TTCTTCTGAGGCTGTGTAATCTCGGACATGTCCTGCTGGAGCAGTCTCAGAGTCACCG	1770
QY	1261	TCCCTGTACCTCAGTGTCTCTCCAGAACTGAGACAAGAAAAGCCCACTCCCTG	1320
DB	1771	TCCCTGTACCTCAGTGTCTCTCCAGAACTGAGACAAGAAAAGCCCACTCCCTG	1830
QY	1321	GATCTTCAATGAACTCAATGGCTACATGTATGATTGGAACAGCAGAGTCTTCGCAAG	1380
DB	1831	GATCTTCAATGAACTCAATGGCTACATGTATGATTGGAACAGCAGAGTCTTCGCAAG	1890

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OM protein - protein search, using sw model

Run on: September 30, 2005, 08:45:06 ; Search time 0.001 Seconds
(without alignments)
230.400 Million cell updates/sec

Title: us-09-402-569-5
Perfect score: 2470
Sequence: 1 MSAEVHQVEEALDTEKEM.....EKYYVWLQHTLRKKLILSYT 480

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 480 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : us-09-009-893a-2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2454	99.4	480	1	us-09-009-893a-2

ALIGNMENTS

RESULT 1
us-09-009-893a-2

Query Match	99.4%;	Score 2454;	DB 1;	Length 480;
Best Local Similarity	99.4%;	Pred. No. 0;		
Matches 477;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1	MSAEVHQVEEALDTEKEMFLC	RDVAIDVVPNNVRLDILRER	GKLSVGDLAELLY 60
Db	1	MSAEVHQVEEALDTEKEMFLC	RDVAIDVVPNNVRLDILRER	GKLSVGDLAELLY 60
QY	61	RVRFDLLKRLKMDRKAVETHLL	RNPVLVSDYRVLMAEIGEDDL	KSDVSSLIIFLMKDYM 120
Db	61	RVRFDLLKRLKMDRKAVETHLL	RNPVLVSDYRVLMAEIGEDDL	KSDVSSLIIFLMKDYM 120
QY	121	GRGKISKEKSFLLVVELEKLN	IVAPDQLLKGKLNHRIIDLTK	IKYKQSVQAGT 180
Db	121	GRGKISKEKSFLLVVELEKLN	IVAPDQLLKGKLNHRIIDLTK	IKYKQSVQAGT 180
QY	181	SYRNVLOAAIQKSLKDPNFR	LHNGRSKEORLKEOLGAQQE	PVKXSIOESEAFIPQSIP 240
Db	181	SYRNVLOAAIQKSLKDPNFR	LHNGRSKEORLKEOLGAQQE	PVKXSIOESEAFIPQSIP 240
QY	241	EERYKMKSPGLGICLIISCI	GNETELLRSFTTSIGYEVOK	FLHLSMHGISQILGQFACMP 300
Db	241	EERYKMKSPGLGICLIISCI	GNETELLRSFTTSIGYEVOK	FLHLSMHGISQILGQFACMP 300

QY	301	EHRDYDSFVCVLVSRGSSQ	SVYGVDOHSGGLPLHHIRRM	FMGDSCPYLAGKPKMPFIQNY 360
Db	301	EHRDYDSFVCVLVSRGSSQ	SVYGVDOHSGGLPLHHIRRM	FMGDSCPYLAGKPKMPFIQNY 360
QY	361	VVSEGOLEDSSILLEVDG	PAMKNVFEKAKRGGLCTVH	READFFWSLCTADMSLLEQSHSSP 420
Db	361	VVSEGOLEDSSILLEVDG	PAMKNVFEKAKRGGLCTVH	READFFWSLCTADMSLLEQSHSSP 420
QY	421	SLYLQCLSQKLRQERKRPL	LLDLHIELNGYMYDMNRSV	SAKEYYVWLQHTLRKKLILSYT 480
Db	421	SLYLQCLSQKLRQERKRPL	LLDLHIELNGYMYDMNRSV	SAKEYYVWLQHTLRKKLILSYT 480

Search completed: September 30, 2005, 08:45:06
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: September 30, 2005, 08:44:29 ; Search time 0.001 Seconds
(without alignments)
230.400 Million cell updates/sec

Title: us-09-402-569-5
Perfect score: 2470
Sequence: 1 MSAEVTHQVEALDTDEKEM.....EKYYVWLQHTLRKKLILSYT 480

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 480 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : us-08-795-088a-2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2454	99.4	480	1/us-08-795-088a-2	

ALIGNMENTS

RESULT 1
us-08-795-088a-2

Query Match	99.4%;	Score	2454;	DB	1;	Length	480;
Best Local Similarity	99.4%;	Pred. No.	0;				
Matches	477;	Conservative	0;	Mismatches	3;	Indels	0;
Gaps	0;						
Qy	1	MSAEVTHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDIAELLY	60				
Db	1	MSAEVTHQVEALDTDEKEMLLFLCRDVAIDVPPNVRDLILRERKLSVGDIAELLY	60				
Qy	61	RVRFDLLKRLKMDRAVTHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYM	120				
Db	61	RVRFDLLKRLKMDRAVTHLLRNPHLVSDYRVLMAEIGEDLDKSDVSSLIIFLMKDYM	120				
Qy	121	GRGKISKEKSFBLVLWVELEKLNVAQDLGLKCLKNHRIIDLTKIKYKQSVQAGT	180				
Db	121	GRGKISKEKSFBLVLWVELEKLNVAQDLGLKCLKNHRIIDLTKIKYKQSVQAGT	180				
Qy	181	SYRNVLOAAIQKSLKDPNNFRLHNGSKQRLKEQLGAQOEVPVKSIQSEAFIPQISIP	240				
Db	181	SYRNVLOAAIQKSLKDPNNFRLHNGSKQRLKEQLGAQOEVPVKSIQSEAFIPQISIP	240				
Qy	241	EEYKMKSKPLGICLIISCIIGNETELLRTSTFTSLGYEVQKFLHLSMHGISQILGQFACMP	300				
Db	241	EEYKMKSKPLGICLIISCIIGNETELLRTSTFTSLGYEVQKFLHLSMHGISQILGQFACMP	300				

Qy 301 EHRDYDSFYCVLVSRGSGSVYGVDOETHSGLPLHHIRRMFMGDCSPYLAKPKMFFIQNY 360
Db 301 EHRDYDSFYCVLVSRGSGSVYGVDOETHSGLPLHHIRRMFMGDCSPYLAKPKMFFIQNY 360
Qy 361 VVSEGOLEDSSLLLEVDGPAMKNVEFKAQKRGGLCTVHREADFFWLSLCTADMSLLEQSHSSP 420
Db 361 VVSEGOLEDSSLLLEVDGPAMKNVEFKAQKRGGLCTVHREADFFWLSLCTADMSLLEQSHSSP 420
Qy 421 SLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWSRVSAKYYVWLQHTLRKKLILSYT 480
Db 421 SLYLQCLSQKLRQERKRPLLDLHIELNGYMYDWSRVSAKYYVWLQHTLRKKLILSYT 480

Search completed: September 30, 2005, 08:44:29
Job time : 0.001 secs

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OM protein - protein search, using sw model

Run on: September 30, 2005, 07:58:49 ; Search time 42 Seconds
(without alignments)
186.623 Million cell updates/sec

Title: US-09-402-569-2

Perfect score: 521

Sequence: 1 KRMSAEVHQVEEALDTDE.....LLRNPHLVSDYRVLMSGE 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCUTS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	504	96.7	221	3	US-09-382-155-17
2	504	96.7	221	3	US-09-074-044A-17
3	504	96.7	445	3	US-08-859-167-2
4	504	96.7	445	3	US-09-109-273-2
5	504	96.7	445	3	US-09-276-993-2
6	504	96.7	445	4	US-09-723-450-2
7	504	96.7	480	3	US-08-795-088A-2
8	504	96.7	480	3	US-09-069-023-34
9	504	96.7	480	4	US-09-009-893A-2
10	504	96.7	480	4	US-09-489-155-2
11	384	73.7	78	3	US-09-382-155-1
12	384	73.7	78	3	US-09-074-044A-1
13	129.5	24.9	139	3	US-09-382-155-20
14	129.5	24.9	139	3	US-09-074-044A-20
15	121.5	23.3	241	3	US-09-382-155-21
16	121.5	23.3	241	3	US-09-074-044A-21
17	119	22.8	371	3	US-09-382-155-22
18	119	22.8	371	3	US-09-074-044A-22
19	113	21.7	79	3	US-09-382-155-9
20	113	21.7	79	3	US-09-074-044A-9
21	109	20.9	79	3	US-09-382-155-3
22	109	20.9	79	3	US-09-074-044A-3
23	102.5	19.7	82	3	US-09-382-155-7
24	102.5	19.7	82	3	US-09-074-044A-7
25	99.5	19.1	79	3	US-09-074-044A-5
26	99.5	19.1	171	3	US-09-382-155-23
27	99.5	19.1	171	3	US-09-074-044A-23

28 98.5 18.9 180 3 US-09-382-155-18 Sequence 18, Appl
29 98.5 18.9 180 3 US-09-074-044A-18 Sequence 18, Appl
30 98.5 18.9 220 2 US-08-807-200-2 Sequence 2, Appl
31 98.5 18.9 220 3 US-09-001-777-2 Sequence 2, Appl
32 98.5 18.9 235 3 US-08-983-502-5 Sequence 5, Appl
33 98.5 18.9 235 4 US-09-516-747-5 Sequence 5, Appl
34 98.5 18.9 235 5 PCT-US96-10521-5 Sequence 5, Appl
35 98.5 18.9 257 1 US-08-618-164-2 Sequence 2, Appl
36 98.5 18.9 261 3 US-08-983-502-25 Sequence 25, Appl
37 98.5 18.9 261 4 US-09-516-747-25 Sequence 25, Appl
38 98.5 18.9 261 5 PCT-US96-10521-25 Sequence 25, Appl
39 98.5 18.9 277 3 US-08-983-502-8 Sequence 8, Appl
40 98.5 18.9 277 4 US-09-516-747-8 Sequence 8, Appl
41 98.5 18.9 277 5 PCT-US96-10521-8 Sequence 8, Appl
42 98.5 18.9 464 3 US-08-983-502-18 Sequence 18, Appl
43 98.5 18.9 464 4 US-09-516-747-18 Sequence 18, Appl
44 98.5 18.9 464 5 PCT-US96-10521-18 Sequence 18, Appl
45 98.5 18.9 478 4 US-09-009-893A-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-382-155-17
; Sequence 17, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; EARLIER FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-155-17

Query Match 96.7%; Score 504; DB 3; Length 221;
Best Local Similarity 99.0%; Pred. No. 2.2e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDLAELLY 63

Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDLAELLY 60

QY 64 RYRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSGE 105

Db 61 RYRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSGE 102

RESULT 2

US-09-074-044A-17
; Sequence 17, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND
; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI

```
/ COUNTRY: USA
/ ZIP: 64108
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/074,044A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: COLLINS, JOHN M
/ REGISTRATION NUMBER: 26,262
/ REFERENCE/DOCKET NUMBER: 26588
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 816/474-9050
/ TELEFAX: 816/474-9057
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 221 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ US-09-074-044A-17

Query Match          96.7%; Score 504; DB 3; Length 221;
Best Local Similarity 99.0%; Pred. No. 2.2e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4  MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDTLRLRGKLSVGDIAELLY 63
DB      1  MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDTLRLRGKLSVGDIAELLY 60

QY      64  RVRRFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
DB      61  RVRRFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102

RESULT 3
US-08-859-167-2
/ Sequence 2, Application US/08859167
/ Patent No. 6037461
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ APPLICANT: Fernandez-Alnemri, Teresa
/ TITLE OF INVENTION: PADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
/ TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
/ TITLE OF INVENTION: OF MAKING THE SAME
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461Iris
/ STREET: One Liberty Place, 46th floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: WINDOWS
/ SOFTWARE: WordPerfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/859,167
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/859,167
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Deluca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 445 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-109-273-2

Query Match          96.7%; Score 504; DB 3; Length 445;
Best Local Similarity 99.0%; Pred. No. 5.1e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4  MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDTLRLRGKLSVGDIAELLY 63
DB      1  MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDTLRLRGKLSVGDIAELLY 60

QY      64  RVRRFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
DB      61  RVRRFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102
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/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 445 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-859-167-2

Query Match          96.7%; Score 504; DB 3; Length 445;
Best Local Similarity 99.0%; Pred. No. 5.1e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4  MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDTLRLRGKLSVGDIAELLY 63
DB      1  MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDTLRLRGKLSVGDIAELLY 60

QY      64  RVRRFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
DB      61  RVRRFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102

RESULT 4
US-09-109-273-2
/ Sequence 2, Application US/09109273
/ Patent No. 6063760
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ APPLICANT: Fernandez-Alnemri, Teresa
/ TITLE OF INVENTION: PADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
/ TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
/ TITLE OF INVENTION: OF MAKING THE SAME
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760Iris
/ STREET: One Liberty Place, 46th floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: WINDOWS
/ SOFTWARE: WordPerfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/109,273
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/859,167
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Deluca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 445 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-109-273-2

Query Match          96.7%; Score 504; DB 3; Length 445;
Best Local Similarity 99.0%; Pred. No. 5.1e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 63
 Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 60
 QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
 Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 5
 US-09-276-993-2
 ; Sequence 2, Application US/09276993
 ; Patent No. 6207801
 ; GENERAL INFORMATION:
 ; APPLICANT: Alnemri, Emad S.
 ; APPLICANT: Fernandez-Alnemri, Teresa
 ; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
 ; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
 ; TITLE OF INVENTION: OF MAKING THE SAME
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
 ; STREET: One Liberty Place, 46th floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: WINDOWS
 ; SOFTWARE: WordPerfect
 ; APPLICATION DATA:
 ; CURRENT APPLICATION NUMBER: US/09/276,993
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/859,167
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DeLuca, Mark
 ; REGISTRATION NUMBER: 33,229
 ; REFERENCE/DOCKET NUMBER: TJU-
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 445 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-276-993-2

Query Match 96.7%; Score 504; DB 3; Length 445;
 Best Local Similarity 99.0%; Pred. No. 5.1e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 63
 Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 60
 QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
 Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 6
 US-09-723-450-2
 ; Sequence 2, Application US/09723450
 ; Patent No. 6576751
 ; GENERAL INFORMATION:
 ; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, And
 ; FILE REFERENCE: TJU2445
 ; CURRENT APPLICATION NUMBER: US/09/723,450
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 09/276,993
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 08/859,167
 ; PRIOR FILING DATE: 1997-05-20
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: No. 6576751el Sequence
 ; US-09-723-450-2

Query Match 96.7%; Score 504; DB 4; Length 445;
 Best Local Similarity 99.0%; Pred. No. 5.1e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 63
 Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 60
 QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
 Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 7
 US-08-795-088A-2
 ; Sequence 2, Application US/08795088A
 ; Patent No. 6242569
 ; GENERAL INFORMATION:
 ; APPLICANT: Sul, Hong-Bing
 ; APPLICANT: Goeddel, David V.
 ; TITLE OF INVENTION: Regulators of Apoptosis
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Science & Technology Law Group
 ; STREET: 75 Denise Drive
 ; CITY: Hillsborough
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94010
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/795,088A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: T97-001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 343-4341
 ; TELEFAX: (650) 343-4342
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 480 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; US-08-795-088A-2

Query Match 96.7%; Score 504; DB 3; Length 480;
Best Local Similarity 99.0%; Pred. No. 5.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDDLRLRERKGLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDDLRLRERKGLSVGDLAELLY 60

QY 64 RVRPFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105

DB 61 RVRPFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 8

US-09-069-023-34
; Sequence 34, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069, 023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-34

Query Match 96.7%; Score 504; DB 3; Length 480;
Best Local Similarity 99.0%; Pred. No. 5.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDDLRLRERKGLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDDLRLRERKGLSVGDLAELLY 60

QY 64 RVRPFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105

DB 61 RVRPFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 9

US-09-009-893A-2
; Sequence 2, Application US/09009893A
; Patent No. 6623938
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Receptor
; TITLE OF INVENTION: CD-95 Induced Apoptosis
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/009, 893A
; CURRENT FILING DATE: 1998-02-21
; PRIOR FILING DATE: 1998-02-21
; PRIOR APPLICATION NUMBER: US 60/054, 800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034, 205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-009-893A-2

Query Match 96.7%; Score 504; DB 4; Length 480;
Best Local Similarity 99.0%; Pred. No. 5.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDDLRLRERKGLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDDLRLRERKGLSVGDLAELLY 60

QY 64 RVRPFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105

DB 61 RVRPFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 10

US-09-489-155-2
; Sequence 2, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Receptor
; TITLE OF INVENTION: CD-95 Induced Apoptosis
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/489, 155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009, 893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034, 205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-155-2

Query Match 96.7%; Score 504; DB 4; Length 480;
Best Local Similarity 99.0%; Pred. No. 5.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDDLRLRERKGLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDDLRLRERKGLSVGDLAELLY 60

QY 64 RVRPFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105

DB 61 RVRPFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 11

US-09-382-155-1
; Sequence 1, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382, 155B
; CURRENT FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074, 044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 78

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-155-1

Query Match      73.7%; Score 384; DB 3; Length 78;
Best Local Similarity 100.0%; Pred. No. 7.7e-38;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNPVRDLILRERKGLSVGDLAELLY 63
Db 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNPVRDLILRERKGLSVGDLAELLY 60

Qy 64 RVRFDLLKRLKMDRKA 81
Db 61 RVRFDLLKRLKMDRKA 78

RESULT 12
US-09-074-044A-1
; Sequence 1, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND APOPTOSIS
; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 26588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-074-044A-1

Query Match      73.7%; Score 384; DB 3; Length 78;
Best Local Similarity 100.0%; Pred. No. 7.7e-38;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNPVRDLILRERKGLSVGDLAELLY 63
Db 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNPVRDLILRERKGLSVGDLAELLY 60

Qy 64 RVRFDLLKRLKMDRKA 81
Db 61 RVRFDLLKRLKMDRKA 78

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RESULT 13
US-09-382-155-20
; Sequence 20, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; CURRENT FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Molluscum contagiosum virus
US-09-382-155-20

Query Match      24.9%; Score 129.5; DB 3; Length 139;
Best Local Similarity 34.0%; Pred. No. 1.3e-07;
Matches 35; Conservative 23; Mismatches 38; Indels 7; Gaps 3;

Qy 7 EVIHQVEALDTDEKEMLLFLCRDVAIDVVPNPVRDLILRERKGLSVGDLAELLY 63
Db 5 EVLCEVARKLGTDDREVLF---LNVFIPQPTLAQLGALRALKEGRITFFLLAECLF 61

Qy 64 RVRFDLLKRLKMDRKA VETHLLRNPHLVSYRVLMSEI-GE 105
Db 62 RAGRDLRLDLHDPFLERHLAGTMSYFSPYQLTVLHV DGE 104

RESULT 14
US-09-074-044A-20
; Sequence 20, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 26588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids

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RESULT 18
US-09-074-044A-22
; Sequence 22, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,044A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 26588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: MOLLUSCUM CONTAGIOSUM VIRUS
US-09-074-044A-22

Query Match 22.8%; Score 119; DB 3; Length 371;
Best Local Similarity 38.8%; Pred. No. 7.3e-06;
Matches 34; Conservative 12; Mismatches 38; Indels 4; Gaps 2;

QY 16 LDTDEKEMLLFLCRDVAIDVPPNVRLDILIRERKGLSVGDLAEILLYRVRFDLKRL 75
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 18 LDASEHEVLFRLCRDVA--PASKTAEDALRALQRRRLTLSSMAELLCALRFRDVLKVR 75
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 76 KMDKAVETHLLRNPHLVSDYRVLMSEI 103
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 GMTRECAGR--LLHGHSFLSQYRLQVAAI 101
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 19
US-09-382-155-9
; Sequence 9, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; CURRENT FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07

US-09-074-044A-9
; Sequence 9, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,044A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 26588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: MOLLUSCUM CONTAGIOSUM VIRUS
US-09-074-044A-9

Query Match 21.7%; Score 113; DB 3; Length 79;
Best Local Similarity 45.3%; Pred. No. 5.5e-06;
Matches 29; Conservative 7; Mismatches 26; Indels 2; Gaps 1;

QY 16 LDTDEKEMLLFLCRDVAIDVPPNVRLDILIRERKGLSVGDLAEILLYRVRFDLKRL 75
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 18 LDASEHEVLFRLCRDVA--PASKTAEDALRALQRRRLTLSSMAELLCALRFRDVLKVR 75
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 76 KMDR 79
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 GMTR 79
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 20
US-09-074-044A-9
; Sequence 9, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,044A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 26588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: MOLLUSCUM CONTAGIOSUM VIRUS
US-09-074-044A-9

Query Match 21.7%; Score 113; DB 3; Length 79;
Best Local Similarity 45.3%; Pred. No. 5.5e-06;
Matches 29; Conservative 7; Mismatches 26; Indels 2; Gaps 1;

QY 16 LDTDEKEMLLFLCRDVAIDVPPNVRLDILIRERKGLSVGDLAEILLYRVRFDLKRL 75
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 18 LDASEHEVLFRLCRDVA--PASKTAEDALRALQRRRLTLSSMAELLCALRFRDVLKVR 75
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 76 KMDR 79
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 GMTR 79
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

US-09-382-155-9
; Sequence 9, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; CURRENT FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
```



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; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,044A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 26588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: MOLLUSCUM CONTAGIOSUM VIRUS
;
US-09-074-044A-7

Query Match 19.7%; Score 102.5; DB 3; Length 82;
Best Local Similarity 42.9%; Pred. No. 9.9e-05;
Matches 27; Conservative 10; Mismatches 23; Indels 3; Gaps 2;

QY 10 HQVEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDIRRGKLSVGDLAELLYRVRRP 69
Db 15 HLLEE-LDSHEDSILLFLCHDAAPGCT--TVTQALCSLSQQRKLTAAALVEMLYVLQRM 71
QY 70 LLK 72
Db 72 LLK 74

RESULT 25
US-09-074-044A-5
; Sequence 5, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,044A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 26588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: MOLLUSCUM CONTAGIOSUM VIRUS
;
US-09-074-044A-5

Query Match 19.1%; Score 99.5; DB 3; Length 79;
Best Local Similarity 39.4%; Pred. No. 0.00021;
Matches 26; Conservative 8; Mismatches 21; Indels 11; Gaps 2;

QY 15 ALDTDEKEMLLFLCRDVAIDVVPPN-----VRDLDIRRGKLSVGDLAELLYRVRRF 68
Db 12 SLDEDETETLYLCRDLL-----KNKGFEQCTRDAPKFLSDYACLSAANQMELLFVGR 66
QY 69 DLLKRI 74
Db 67 DLIRRI 72

RESULT 26
US-09-382-155-23
; Sequence 23, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; CURRENT FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Equine Herpesvirus
;
US-09-382-155-23

Query Match 19.1%; Score 99.5; DB 3; Length 171;
Best Local Similarity 39.4%; Pred. No. 0.00055;
Matches 26; Conservative 8; Mismatches 21; Indels 11; Gaps 2;

QY 15 ALDTDEKEMLLFLCRDVAIDVVPPN-----VRDLDIRRGKLSVGDLAELLYRVRRF 68
Db 12 SLDEDETETLYLCRDLL-----KNKGFEQCTRDAPKFLSDYACLSAANQMELLFVGR 66
QY 69 DLLKRI 74
Db 67 DLIRRI 72

RESULT 27
US-09-074-044A-23
; Sequence 23, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
```

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/ TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
/ TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
/ NUMBER OF SEQUENCES: 28
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
/ STREET: 2405 GRAND BLVD., SUITE 400
/ CITY: KANSAS CITY
/ STATE: MISSOURI
/ COUNTRY: USA
/ ZIP: 64108
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/074,044A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: COLLINS, JOHN M
/ REGISTRATION NUMBER: 26,262
/ REFERENCE/DOCKET NUMBER: 26588
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 816/474-9057
/ TELEFAX: 816/474-9057
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 171 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Equine herpesvirus
/
/ US-09-074-044A-23
/
/ Query Match 19.1%; Score 99.5; DB 3; Length 171;
/ Best Local Similarity 39.4%; Pred. No. 0.00055;
/ Matches 26; Conservative 8; Mismatches 21; Indels 11; Gaps 2;
/
/ QY 15 ALDTEKEMLLFLCRDVAIDVVPPN-----VRDLDDILRERKLSVGDLAELLYRVRRF 68
/ Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
/ 12 SLDEDETETVLCRDLL-----KNKGFCQTRDAFKFLSDYACLSAANQMELLFRVGR 66
/
/ QY 69 DLLKRI 74
/ Db |||:|||||
/ 67 DLIRRI 72
/
/ RESULT 28
/ US-09-382-155-18
/ ; Sequence 18, Application US/09382155B
/ ; Patent No. 6160095
/ ; GENERAL INFORMATION:
/ ; APPLICANT: CHAUDHARY, PREET M
/ ; APPLICANT: HOOD, LEROY
/ ; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
/ ; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
/ ; FILE REFERENCE: Chaudhary
/ ; CURRENT APPLICATION NUMBER: US/09/382,155B
/ ; CURRENT FILING DATE: 1999-08-24
/ ; EARLIER APPLICATION NUMBER: 09/074,044
/ ; EARLIER FILING DATE: 1998-05-07
/ ; NUMBER OF SEQ ID NOS: 40
/ ; SOFTWARE: PatentIn Ver. 2.1
/ ; SEQ ID NO 18
/ ; LENGTH: 180
/ ; TYPE: PRT
/ ; ORGANISM: Homo sapiens
/
/ US-09-382-155-18
/
/ Query Match 18.9%; Score 98.5; DB 3; Length 180;
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Best Local Similarity 29.4%; Pred. No. 0.00077;
Matches 32; Conservative 26; Mismatches 34; Indels 17; Gaps 6;
/
/ QY 9 THQVEALDTEKEMLLFLCRDVAIDVVPPN-----VRDLDDI---LRERKLSVGDLA-- 59
/ Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
/ 7 LYDIGEQDSEDLASLKFL-----SLDYIPQRKQEPFKDALMLFQRLQEKRMLEESNLSFL 62
/
/ QY 60 -ELLYRVRRFDLLKRLKMDRKAVETHLLRNP--HLVSDYRVLMSEIGE 105
/ Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
/ 63 KELLFRINRLDLLITYLNTRKEEMERE-LQTPGRAQISAYRVMLYQISE 110
/
/ RESULT 29
/ US-09-074-044A-18
/ ; Sequence 18, Application US/09074044A
/ ; Patent No. 6207458
/ ; GENERAL INFORMATION:
/ ; APPLICANT: CHAUDHARY, PREET M
/ ; APPLICANT: HOOD, LEROY
/ ; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
/ ; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
/ ; NUMBER OF SEQUENCES: 28
/ ; CORRESPONDENCE ADDRESS:
/ ; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
/ ; STREET: 2405 GRAND BLVD., SUITE 400
/ ; CITY: KANSAS CITY
/ ; STATE: MISSOURI
/ ; COUNTRY: USA
/ ; ZIP: 64108
/ ; COMPUTER READABLE FORM:
/ ; MEDIUM TYPE: Floppy disk
/ ; COMPUTER: IBM PC compatible
/ ; OPERATING SYSTEM: PC-DOS/MS-DOS
/ ; SOFTWARE: PatentIn Release #1.0, Version #1.30
/ ; CURRENT APPLICATION DATA:
/ ; APPLICATION NUMBER: US/09/074,044A
/ ; FILING DATE:
/ ; CLASSIFICATION: 435
/ ; ATTORNEY/AGENT INFORMATION:
/ ; NAME: COLLINS, JOHN M
/ ; REGISTRATION NUMBER: 26,262
/ ; REFERENCE/DOCKET NUMBER: 26588
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: 816/474-9050
/ ; TELEFAX: 816/474-9057
/ ; INFORMATION FOR SEQ ID NO: 18:
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 180 amino acids
/ ; TYPE: amino acid
/ ; STRANDEDNESS:
/ ; TOPOLOGY: not relevant
/ ; MOLECULE TYPE: protein
/ ; ORIGINAL SOURCE:
/ ; ORGANISM: Homo sapiens
/
/ US-09-074-044A-18
/
/ Query Match 18.9%; Score 98.5; DB 3; Length 180;
/ Best Local Similarity 29.4%; Pred. No. 0.00077;
/ Matches 32; Conservative 26; Mismatches 34; Indels 17; Gaps 6;
/
/ QY 9 THQVEALDTEKEMLLFLCRDVAIDVVPPN-----VRDLDDI---LRERKLSVGDLA-- 59
/ Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
/ 7 LYDIGEQDSEDLASLKFL-----SLDYIPQRKQEPFKDALMLFQRLQEKRMLEESNLSFL 62
/
/ QY 60 -ELLYRVRRFDLLKRLKMDRKAVETHLLRNP--HLVSDYRVLMSEIGE 105
/ Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
/ 63 KELLFRINRLDLLITYLNTRKEEMERE-LQTPGRAQISAYRVMLYQISE 110
/
/ RESULT 30
/ US-08-807-200-2
/ ; Sequence 2, Application US/08807200
/ ; Patent No. 5837837
```

```

; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shigjan, Andrew W.
; APPLICANT: Wong, Grace H.W.
; TITLE OF INVENTION: NOVEL FORMS OF CASPASE-8 AND
; TITLE OF INVENTION: USES THEREFOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/807,200
; FILING DATE: 27-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/021001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-807-200-2

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```

Query Match      18.9%; Score 98.5; DB 2; Length 220;
Best Local Similarity 29.4%; Pred. No. 0.00098;
Matches 32; Conservative 26; Mismatches 34; Indels 17; Gaps 6;

QY 9 IHOVERALDTDEKEMLLFLCRDVAIDVWPN---VRDLLDI--LRERKLSVGDLA-- 59
Db 7 LYDIGQLDSEDLASKFL---SLDYIPORKOEPIKDMLFQERKMLEESNLSFL 62

QY 60 -ELLYRVRFPDLLKRLKMDKAVETHLLRNP--HLVSDYRVLMSIGE 105
Db 63 KELLFRINRLDLITYLNTKREMERERE-LQTPGQAQISAYRWMLYQISE 110

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Search completed: September 30, 2005, 08:02:43
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: September 30, 2005, 07:58:45 ; Search time 71 Seconds
(without alignments)

571.970 Million cell updates/sec

Title: us-09-402-569-2

Perfect score: 521

Sequence: 1 KRMSAEVHQVEEALDTDE.....LLRNPHLVSDRYVLMSEIGE 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	516	99.0	104	2	AAW76215 Human FLI
2	506	97.1	491	3	AAAB03964 FLIP with
3	504	96.7	221	2	AAW78904 Human G1
4	504	96.7	221	2	AAW76630 Human CFL
5	504	96.7	221	2	AAW05789 Human MAC
6	504	96.7	221	2	AAW57455 Human FLI
7	504	96.7	221	3	AAW03959 FLICE-lik
8	504	96.7	221	4	AAW61117 Human MRI
9	504	96.7	221	4	AAW84802 Human MRI
10	504	96.7	221	5	AAW09293 Human FLI
11	504	96.7	227	2	AAW05795 MRIT beta
12	504	96.7	270	5	AAW26110 Human FLA
13	504	96.7	291	3	AAW67420 Usurpin-g
14	504	96.7	445	2	AAW90107 Human FLA
15	504	96.7	445	5	AAW26086 Human FLA
16	504	96.7	462	3	AAW67419 Usurpin-b
17	504	96.7	462	8	ADRI4101 Human NF-
18	504	96.7	480	2	AAW58578 Human PIN
19	504	96.7	480	2	AAW69715 Human Cas
20	504	96.7	480	2	AAW69229 I-FLICE-1
21	504	96.7	480	2	AAW78903 Human CFL
22	504	96.7	480	2	AAW76631 Human CFL
23	504	96.7	480	2	AAW05787 Human MAC
24	504	96.7	480	2	AAW57454 Human FLI
25	504	96.7	480	3	AAW59414 Human CLA

26	504	96.7	480	3	AAW57606 Human apo
27	504	96.7	480	3	AAW67418 Usurpin-a
28	504	96.7	480	3	AAAB03960 FLICE-lik
29	504	96.7	480	5	AAW09294 Human FLI
30	504	96.7	480	7	ADA10615 Human inh
31	504	96.7	480	7	ADJ68469 Human hea
32	504	96.7	480	7	ADN95807 Human BEC
33	504	96.7	480	8	ADJ96510 Human I-F
34	504	96.7	480	8	ADRI1312 Human inh
35	504	96.7	480	8	ADP54877 Human PRO
36	488.5	93.8	479	2	AAW76625 Human FLI
37	465	89.3	93	4	AAW16659 Peptide #
38	465	89.3	93	4	ABW35643 Peptide #
39	465	89.3	93	4	AAW29143 Peptide #
40	465	89.3	93	4	ABB30476 Peptide #
41	465	89.3	93	4	ABB21072 Protein #
42	465	89.3	93	4	AAW68836 Human bon
43	465	89.3	93	4	AAW56459 Human bra
44	465	89.3	93	4	ABG50496 Human liv
45	465	89.3	93	4	AAW04375 Peptide #

ALIGNMENTS

RESULT 1

AAW76215
ID AAW76215 standard; protein; 104 AA.

XX AAW76215;

DT 26-NOV-1998 (first entry)

DE Human FLIP protein.

KW FLIP; FLICE inhibitory protein; human; apoptosis-inhibiting protein;

KW protease; death-inducing signalling complex; apoptosis; diagnosis; AIDS;

KW acquired immune deficiency syndrome; neurodegenerative disease.

XX Homo sapiens.

XX DE19713434-C1.

PD 24-SEP-1998.

PF 01-APR-1997; 97DE-01013434.

PR 01-APR-1997; 97DE-01013434.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Krammer P, Peter M, Scaffidi C;

XX WPI; 1998-482168/42.

DR N-PSDB; AAW46493.

XX Apoptosis-inhibiting FLIP protein and corresponding DNA - useful for inhibiting or diagnosing apoptosis.

PS Claim 1; Fig 1; 5pp; German.

CC This sequence represents a human apoptosis-inhibiting protein, FLIP (FLICE inhibitory protein). FLICE is a protease involved in the death-inducing signalling complex. This protein can be used to inhibit apoptosis and the DNA can be used to diagnose and/or inhibit apoptosis, especially where the apoptosis is associated with AIDS or neurodegenerative diseases

XX Sequence 104 AA;

Query Match 99.0%; Score 516; DB 2; Length 104;

Best Local Similarity 100.0%; Pred.No. 5.5e-53;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC or inflammatory processes. (II) is used to inhibit cell death, and its
 CC inhibitors augment/enhance the processes. (I) and (II) regulate the PAS-R
 CC ligand or TNF effect on cells carrying an FAS-R or p55-R. Tumour, HIV-
 CC infected or other diseased cells can be treated using a viral vector
 CC encoding a viral surface protein, which binds a specific cell surface
 CC receptor and a sequence encoding (II), which kills the cell. Antisense
 CC oligonucleotides, introduced using the above vector, block the expression
 CC of (II) and can also regulate the above effects. These effects can also
 CC be regulated using a vector encoding a ribozyme that interacts with a
 CC cellular mRNA encoding (II), and allows (II) expression
 XX
 SQ Sequence 221 AA;

Query Match 96.7%; Score 504; DB 2; Length 221;
 Best Local Similarity 99.0%; Pred. No. 3.7e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLTLRERKLSVGDIAELLY 63
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLTLRERKLSVGDIAELLY 60
 QY 64 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIEGE 105
 DB 61 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 4
 AA76630
 ID AA76630 standard; protein; 221 AA.

XX AA76630;
 AC
 XX
 DT 12-JUL-1999 (first entry)
 DE Human CFLIP-S protein.
 DE
 KW Death effector domain; human; murine; anti-apoptotic; treatment;
 KW HIV infection; autoimmune disease; FLIP protein.
 XX

OS Homo sapiens.
 XX
 PN DE19713393-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 01-APR-1997; 97DE-01013393.
 XX
 PR 01-APR-1997; 97DE-01013393.
 XX
 PA (TSCH/) TSCHOPP J.
 XX
 PI Tschopp J, Thome M, Burns K, Irmeler M, Hahne M, Schroeter M;
 PI Schneider P, Bodmer J, Steiner V, Rimoldi D, Hoffmann K, French EL;
 XX
 DR WPI; 1998-532710/46.
 DR N-PSDB; AAV61936.
 XX
 XX New DNA encoding for anti-apoptotic gene product - used to treat HIV
 PT infections and autoimmune diseases.
 PT
 PS Claim 20; Fig 4A; 45pp; German.

XX This invention describes novel human and mouse anti-apoptotic gene
 CC products which contain at least one death effector domain. The products
 CC of the invention are used in the treatment of HIV infections and
 CC autoimmune diseases
 CC
 SQ Sequence 221 AA;

Query Match 96.7%; Score 504; DB 2; Length 221;
 Best Local Similarity 99.0%; Pred. No. 3.7e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLTLRERKLSVGDIAELLY 63
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLTLRERKLSVGDIAELLY 60
 QY 64 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIEGE 105
 DB 61 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 5
 AA505789
 ID AA505789 standard; protein; 221 AA.

XX AA505789;
 AC
 XX
 DT 02-AUG-1999 (first entry)
 DE Human MACH related inducer of toxicity MRIT beta 1.
 DE
 KW MRIT beta 1; MACH related inducer of toxicity; human; apoptosis;
 KW pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
 KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
 KW aplastic anaemia; myocardial infarction; therapy.
 XX

OS Homo sapiens.
 XX
 PN WO9918230-A2.
 XX
 PD 15-APR-1999.
 XX

PF 07-OCT-1998; 98WO-US021132.
 XX
 PR 07-OCT-1997; 97US-00946226.
 XX
 XX (UNIW) UNIV WASHINGTON.
 PA
 PI Chaudhary PM;

XX
 DR WPI; 1999-277275/23.
 DR N-PSDB; AAX25510.
 XX

XX Identifying regulators of MACH-related inducer of toxicity.

XX Example 1; Fig 1H; 78pp; English.

XX The present sequence represents novel human MACH-related inducer of
 CC toxicity (MRIT) isoform MRIT beta 1, a CED-4 homologue. Multiple isoforms
 CC of MRIT have been identified, some of which function to induce caspase
 CC dependent apoptosis in mammalian cells, e.g. MRIT alpha 1 (see AAY05787)
 CC and MRIT beta 1, while others have anti-apoptotic activity, e.g. MRIT
 CC alpha 2 (see AAY05788). MRIT beta 1 lacks the N-terminal death effector
 CC domain of MRIT alpha 1 but includes a C-terminal caspase ICE homology
 CC domain region. Selective enhancers and inhibitors of MRIT apoptotic
 CC activity can be identified and used to treat diseases mediated by the
 CC dysfunction of programmed cell death or proliferation. A cell
 CC accumulation disorder such as cancer, autoimmune disease, viral
 CC infection, angiogenesis or atherosclerosis is treated by administering an
 CC agent that selectively enhances MRIT apoptotic activity, thereby inducing
 CC apoptosis in a subject. A disorder of cell loss, such as a
 CC neurodegenerative disorder, including Alzheimer's disease, Parkinson's
 CC disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial
 CC infarction or AIDS can be treated by administering an agent that
 CC selectively inhibits MRIT apoptotic activity
 XX

SQ Sequence 221 AA;

Query Match 96.7%; Score 504; DB 2; Length 221;
 Best Local Similarity 99.0%; Pred. No. 3.7e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLTLRERKLSVGDIAELLY 63
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLTLRERKLSVGDIAELLY 60

Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERGKLSVGDLAELLY 60

QY 64 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
|||||

Db 61 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
|||||

RESULT 6
AAY57455
ID AAY57455 standard; protein; 221 AA.
AC AAY57455;
XX
DT 25-FEB-2000 (first entry)
XX
DE Human FLICE-like inhibitory protein short form protein sequence.
XX
KW Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;
KW FLICE-like inhibitory protein short form; apoptosis inhibitor;
KW arteriosclerosis; vascular wall inflammation; vascular injury;
KW Fas ligand-mediated apoptosis; atherosclerosis; transplant.
XX
OS Homo sapiens.
PN WO9942570-A1.
XX
PD 26-AUG-1999.
XX
PF 19-FEB-1999; 99WO-US003558.
XX
PR 20-FEB-1998; 98US-0075471P.
XX
PA (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
XX
PI Walsh K;
XX
DR WPI; 1999-527469/44.
DR N-PSDB; AA239041.
XX
PT Treating conditions characterized by vascular wall inflammation.
XX
PS Example 2; Page 72; 105pp; English.
XX
CC The present sequence represents human FLICE-like inhibitory protein short
CC form, designated FLIP-S. The present invention describes a new treatment
CC of a condition characterised by vascular wall inflammation in a subject
CC comprising administering a Flap molecule to inhibit Fas ligand-mediated
CC apoptosis of vascular endothelial cells in the subject. The method can be
CC used to treat atherosclerosis, transplant arteriosclerosis and vascular
CC injury
XX
SQ Sequence 221 AA;

Query Match 96.7%; Score 504; DB 2; Length 221;
Best Local Similarity 99.0%; Pred. No. 3.7e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERGKLSVGDLAELLY 63
|||||

Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERGKLSVGDLAELLY 60
|||||

QY 64 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
|||||

Db 61 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
|||||

RESULT 7
AAB03959
ID AAB03959 standard; protein; 221 AA.
XX
AC AAB03959;
XX
DT 26-FEB-2001 (first entry)

XX FLICE-like inhibitor protein (Genbank Accession No. 2253681).
DE Chimeric protein; fusion protein; FLICE like inhibitor protein; FLIP;
KW Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
KW tumour specific antigen; immune response; therapy; prophylaxis;
KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;
KW acquired immune deficiency syndrome; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200059935-A1.
XX
PD 12-OCT-2000.
XX
PF 05-APR-2000; 2000WO-US009002.
XX
PR 05-APR-1999; 99US-0127867P.
PR 06-APR-1999; 99US-0128021P.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PA (PAYA/) PAYA C.
PA (ALGE/) ALGECIRAS-SCHMINICH A.
XX
PI Paya C, Algeciras-Schminich A;
XX
DR WPI; 2000-664988/64.
XX
PT Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
PT comprises portion of anti-apoptotic polypeptide linked to a transport
PT group.
XX
PS Disclosure; Page 78-79; 89pp; English.
XX
CC A chimeric group or fusion peptide which comprises a portion of an anti-
CC apoptotic polypeptide which inhibits apoptosis of lymphocytes in
CC combination with a transport group is described. The transport group is
CC capable of transporting the chimeric group or fusion peptide across the
CC cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor
CC protein (FLIP) which inhibits Fas and TNF mediated apoptosis by
CC inhibiting binding of Caspase-8 to the Fas receptor complex, thus
CC shutting off the downstream Fas signalling pathway. The chimeric group
CC and fusion peptide are useful for inhibiting ligand-induced apoptosis by
CC bringing them into contact with T cells. The chimeric group is useful for
CC expanding T cells in vitro e.g. T cells specific for particular antigens
CC such as tumour-specific antigen, for enhancing immune response and to
CC inhibit the apoptosis of chronically activated T cells e.g. activated
CC CD4+ T cells in HIV infected patients. The chimeric group is also useful
CC for therapeutic, prophylactic or diagnosis of intracellular delivery of
CC small molecules and macromolecules such as anti-apoptotic polypeptides
CC and nucleic acids encoding such polypeptides
XX
SQ Sequence 221 AA;

Query Match 96.7%; Score 504; DB 3; Length 221;
Best Local Similarity 99.0%; Pred. No. 3.7e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERGKLSVGDLAELLY 63
|||||

Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERGKLSVGDLAELLY 60
|||||

QY 64 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
|||||

Db 61 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
|||||

RESULT 8
AAB61117
ID AAB61117 standard; protein; 221 AA.
XX
AC AAB61117;


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XX 02-MAY-2001 (first entry)
XX Human MRITalpha.
XX Human; MRITalpha; apoptotic; nuclear factor-kappa B; NF-kB;
XX Jun N-terminal kinase; JUNK; apoptosis; Caspase-8 mutant.
XX Homo sapiens.
XX US6160095-A.
XX 12-DEC-2000.
XX 24-AUG-1999; 99US-00382155.
XX 07-MAY-1998; 98US-00074044.
XX (UNIW ) UNIV WASHINGTON.
XX (STOW-) STOWERS INST MEDICAL RES.
XX Hood L, Chaudhary PM;
XX WPI; 2001-101569/11.
XX Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
XX nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
XX for therapeutic purposes.
XX Example 8; Col 43-46; 60pp; English.
XX The present sequence has been shown to regulate the nuclear factor-kappa
XX B (NF-kB), Jun N-terminal kinase (JUNK) and apoptosis pathways. It is
XX provided in a specification relating to novel mutants (D73A, L74A and
XX L75A) for Caspase-8, which are also useful for regulating NF-kB, JUNK and
XX apoptosis activities. The Caspase-8 mutants are useful for therapeutic
XX purposes and in test methods or assays for determining whether a
XX candidate compound has a significant effect upon cell activities,
XX especially NF-kB, JUNK and apoptosis, so as to facilitate the discovery
XX and/or design of therapeutic agents
XX Sequence 221 AA;

Query Match 96.7%; Score 504; DB 4; Length 221;
Best Local Similarity 99.0%; Pred. No. 3.7e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDDLRLRERKLSVGDIAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDDLRLRERKLSVGDIAELLY 60

QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 9
AAB84802
ID AAB84802 standard; protein; 221 AA.
AC AAB84802;
XX 12-JUL-2001 (first entry)
XX Huamn MRIT prodomain.
XX NF-kappaB; JNK; apoptosis; death effector domain; DED.
XX Homo sapiens.
XX US6207458-B1.
XX 27-MAR-2001.

Query Match 96.7%; Score 504; DB 4; Length 221;
Best Local Similarity 99.0%; Pred. No. 3.7e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDDLRLRERKLSVGDIAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDDLRLRERKLSVGDIAELLY 60

QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 10
AEB09293
ID AEB09293 standard; protein; 221 AA.
AC AEB09293;
XX 15-JUL-2002 (first entry)
XX Human FLIP-c protein SEQ ID NO:10.
XX Human; FLIP-c; caspase 8 dominant negative regulator; antiinflammatory;
XX anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;
XX phosphorothioate; antisense modulation; infection; inflammation; tumour.
XX Homo sapiens.
XX WO200224717-A1.
XX 28-MAR-2002.
XX 14-SEP-2001; 2001WO-US028732.
XX 20-SEP-2000; 2000US-00666269.
XX (ISIS-) ISIS PHARM INC.
XX Ackermann EJ, Bennett CF, Zhang H, Watt AT, Ricketts W, Dean NM;
XX WPI; 2002-404948/43.
XX N-PSDB; ABL52332.
XX Novel antisense compound that hybridizes and inhibits nucleic acid

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XX 07-MAY-1998; 98US-00074044.
XX 07-MAY-1998; 98US-00074044.
XX (UNIW ) UNIV WASHINGTON.
XX Chaudhary PM, Hood L;
XX WPI; 2001-342087/36.
XX Testing candidate compound affecting cellular NFkappaB JNK, apoptosis
XX activity by comparing cell activity in presence and absence of
XX proteinaceous species having two death effector domain and test compound.
XX Disclosure; Col 47-50; 62pp; English.
XX The present invention relates to testing candidate compounds to determine
XX whether they affect NF-kappaB, JNK and apoptosis activity. The method
XX involves the use of 2 death effector domains (DED). The compounds
XX identified by the invention have therapeutic applications and are useful
XX for regulating cellular NFkappaB, JNK and apoptosis activity. The assay
XX is useful for identifying pharmacological agents or lead compounds
XX generally involved in assaying for compounds which regulate or modulate a
XX cell activity. The present sequence is a prodomain used in the invention
XX Sequence 221 AA;

Query Match 96.7%; Score 504; DB 4; Length 221;
Best Local Similarity 99.0%; Pred. No. 3.7e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDDLRLRERKLSVGDIAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDDLRLRERKLSVGDIAELLY 60

QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 10
AEB09293
ID AEB09293 standard; protein; 221 AA.
AC AEB09293;
XX 15-JUL-2002 (first entry)
XX Human FLIP-c protein SEQ ID NO:10.
XX Human; FLIP-c; caspase 8 dominant negative regulator; antiinflammatory;
XX anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;
XX phosphorothioate; antisense modulation; infection; inflammation; tumour.
XX Homo sapiens.
XX WO200224717-A1.
XX 28-MAR-2002.
XX 14-SEP-2001; 2001WO-US028732.
XX 20-SEP-2000; 2000US-00666269.
XX (ISIS-) ISIS PHARM INC.
XX Ackermann EJ, Bennett CF, Zhang H, Watt AT, Ricketts W, Dean NM;
XX WPI; 2002-404948/43.
XX N-PSDB; ABL52332.
XX Novel antisense compound that hybridizes and inhibits nucleic acid

```

PT encoding a natural dominant negative regulator of caspase 8, FLIP-c,
PT useful for preventing or delaying infection, inflammation or tumor
PT formation.
PS
XX Example 13; Page 116-117; 154pp; English.
XX
CC The present invention describes a compound (I) 8-50 nucleobases in length
CC targeted to a nucleic acid molecule (II) encoding a natural dominant
CC negative regulator of caspase 8, FLIP-c, where (II) specifically
CC hybridizes with and inhibits expression of the protein, or specifically
CC hybridizes with at least an 8-nucleobase portion of an active site on
CC (III). (I) has antinflammatory and anti-tumour activities. (I) is an
CC inhibitor of FLIP-c expression, a modulator of apoptosis and can be used
CC in antisense gene therapy. (I) is useful for inhibiting the expression of
CC FLIP-c in cells or tissues, and for treating an animal having a disease
CC or condition associated with FLIP-c. (I) is also useful for modulating
CC apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or
CC caspase 7 is activated, and the FLIP-c is the long form of FLIP-c. (I) is
CC also useful for diagnostics, therapeutics, prophylaxis, as research
CC reagents and kits, for distinguishing functions of various members of a
CC biological pathway, and in antisense gene therapy. (I) is also useful
CC prophylactically, e.g., to prevent or delay infection, inflammation or
CC tumour formation. The present sequence represents human FLIP-c as given
CC in an example from the present invention
XX
SQ Sequence 221 AA;

Query Match 96.7%; Score 504; DB 5; Length 221;
Best Local Similarity 99.0%; Pred. No. 3.7e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERKLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERKLSVGDLAELLY 60
QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 11
AA05795
ID AAY05795 standard; protein; 227 AA.
AC AAY05795;
XX
DT 02-AUG-1999 (first entry)
XX
DE MRIT beta 2 polypeptide.
XX
KW MRIT beta 2; MACH related inducer of toxicity; human; apoptosis;
KW anti-apoptotic; cancer; autoimmune disease; angiogenesis;
KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;
KW aplastic anaemia; myocardial infarction; therapy; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9918230-A2.
XX
XX 15-APR-1999.
XX
PF 07-OCT-1998; 98WO-US021132.
XX
PR 07-OCT-1997; 97US-00946226.
XX
XX (UNIW) UNIV WASHINGTON.
PA
PI Chaudhary PM;
XX
XX WPI; 1999-277275/23.
DR
XX

PT Identifying regulators of MACH-related inducer of toxicity.
XX
PS Example 2; Page; 78pp; English.
XX
CC The present sequence represents MRIT beta 2, comprising amino acid
CC residues 1-227 of novel human MACH-related inducer of toxicity MRIT alpha
CC 1 (see AAY05787). This deletion mutant was used to examine the
CC interaction of MRIT alpha 1 with caspases. The results indicated that the
CC C-terminal 216 residues of MRIT are not sufficient for FLICE-p20
CC interaction. The invention provides multiple isoforms of MRIT (see
CC AAY05787-89), isolated active fragments of which have either pro-
CC apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors
CC of MRIT apoptotic activity can be identified and used to treat diseases
CC mediated by the dysfunction of programmed cell death or proliferation,
CC such as cancer or a neurodegenerative disorder. Note: the present
CC sequence is not shown in the specification but is derived from the MRIT
CC alpha 1 sequence given in figure 1F
XX
SQ Sequence 227 AA;

Query Match 96.7%; Score 504; DB 2; Length 227;
Best Local Similarity 99.0%; Pred. No. 3.8e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERKLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERKLSVGDLAELLY 60
QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 12
AAE26110
ID AAE26110 standard; protein; 270 AA.
XX
AC AAE26110;
XX
DT 14-NOV-2002 (first entry)
XX
DE Human FLAME-1b protein.
XX
KW Human; FADD-like apoptotic/anti-apoptotic protein; Alzheimer's disease;
KW gene therapy; human immunodeficiency virus; HIV infection; apoptosis;
KW FLAME-1b.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 232..270
FT /note= "FLAME-1b unique region"
XX
PN US2002086983-A1.
XX
PD 04-JUL-2002.
XX
PF 22-AUG-2001; 2001US-00935223.
XX
PR 28-OCT-1997; 97US-00959167.
PR 26-MAR-1999; 99US-00276993.
PR 28-NOV-2000; 2000US-00723450.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Alnemri ES;
XX
DR WPI; 2002-642259/69.
XX
PT Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting
PT apoptosis, treating diseases characterized by apoptosis e.g. HIV
PT infection and Alzheimer's disease, and for identifying modulators of the
PT protein.

XX Example; Fig 1A; 35pp; English.

XX The invention relates to FADD-like apoptotic/anti-apoptotic proteins

CC (FLAME 1 or 2) and nucleic acid molecules encoding such proteins. FLAME

CC sequences are useful for inhibiting apoptosis and for gene therapy of

CC diseases characterised by apoptosis including HIV infection and

CC Alzheimer's disease. FLAME inhibitors are useful as apoptotic agents and

CC activators are useful as anti-apoptotic agents. FLAME-1 is useful as a

CC substrate for caspase in assays to identify caspase inhibitors. The

CC present sequence is human FLAME-1b protein

XX Sequence 270 AA;

Query Match 96.7%; Score 504; DB 5; Length 270;

Best Local Similarity 99.0%; Pred. No. 4.7e-51;

Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVTHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERGLKSLVGDIAELLY 63

DB 1 MSAEVTHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERGLKSLVGDIAELLY 60

QY 64 RVRFPDLKRLKMDKAVETHLLRNPHLVSDYRVLMAEIGE 105

DB 61 RVRFPDLKRLKMDKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 13

AAV67420

ID AAV67420 standard; protein; 291 AA.

XX

AC AAV67420;

XX

DT 12-MAY-2000 (first entry)

XX

DE Usurpin-gamma polypeptide.

XX

KW Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;

KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;

KW caspase; cytostatic; antiParkinsonian; antidiabetic.

XX

OS Homo sapiens.

XX

FN WO200003023-A1.

XX

XX 20-JAN-2000.

XX

XX 07-JUL-1999; 99WO-CA000615.

XX

PR 08-JUL-1998; 98US-0092005P.

XX

PA (MERI) MERCK FROSST CANADA INC.

XX

PI Nicholson DM, Rasper DM, Xanthoudakis S, Roy S;

XX

DR WPI; 2000-160929/14.

DR N-PSDB; AA256989.

XX

PT Novel recombinant DNA molecules and polypeptides for treating apoptosis

PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's

PT disease.

XX

XX Claim 6; Fig 11B; 69pp; English.

XX

CC The invention provides recombinant nucleic acid molecules encoding

CC usurpin-alpha (lacking the first death effector domain (DED) or its

CC prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are

CC useful for in vitro and in vivo identification of usurpin-procaspase-8

CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity

CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis

CC is useful for treating diseases like autoimmune diabetes, cancer and

CC Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8

CC interaction are also useful for treating various diseases mediated by

CC apoptosis. Usurpin provides an attractive model for modulating caspase

CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be

CC regulated at several levels in the presence of usurpin, conferring

CC resistance to Fas-ligand cell death. The present sequence represents the

CC usurpin-gamma polypeptide

XX

SQ Sequence 291 AA;

Query Match 96.7%; Score 504; DB 3; Length 291;

Best Local Similarity 99.0%; Pred. No. 5.2e-51;

Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVTHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERGLKSLVGDIAELLY 63

DB 1 MSAEVTHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLILRERGLKSLVGDIAELLY 60

QY 64 RVRFPDLKRLKMDKAVETHLLRNPHLVSDYRVLMAEIGE 105

DB 61 RVRFPDLKRLKMDKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 14

AAW90107

ID AAW90107 standard; protein; 445 AA.

XX

AC AAW90107;

XX

DT 12-APR-1999 (first entry)

XX

DE Human FLAME-1 protein.

XX

KW FLAME-1; FADD-like apoptotic/anti-apoptotic molecule; human; apoptosis;

KW HIV; infection; Alzheimer's disease; cancer; therapy.

XX

OS Homo sapiens.

XX

FT Key

FT Domain 1. .341

FT Region 5. .71

FT Region 90. .168

FT Region 197. .445

FT Region 322. .327

FT Active-site 338. .342

FT Cleavage-site 342. .445

FT Domain

XX

XX WO9852963-A1.

XX

XX 26-NOV-1998.

XX

XX 20-MAY-1998; 98WO-US010200.

XX

XX 20-MAY-1997; 97US-00859167.

XX

XX (UYJB-) UNIV JEFFERSON THOMAS.

XX

XX Alnemri ES;

XX

XX WPI; 1999-045296/04.

DR N-PSDB; AAV74136.

XX

PT New isolated FADD-like anti-apoptotic molecules - used to develop

PT apoptotic and anti-apoptotic agents for treating, e.g. HIV infection,

PT Alzheimer's disease or neoplastic conditions.

XX

PS Claim 2; Page 39-40; 68pp; English.

XX

CC This is the amino acid sequence of human FLAME-1, or FADD-like
 CC apoptotic/anti-apoptotic molecule 1. FLAME-1 is a novel anti-apoptotic
 CC protein that interacts specifically with FADD, Mch4, Mch5 and FLAME-2. It
 CC is recruited to the Fas receptor complex and can abrogate Fas/TNF-induced
 CC apoptosis upon expression in Fas/TNF-sensitive MCF-7 cells. Despite
 CC having a caspase domain-like region, it does not have caspase activity.
 CC The amino acid sequence of FLAME-1 was deduced from the nucleotide
 CC sequence (see AAV74136) of a Jurkat cell-derived cDNA clone. Host cells,
 CC recombinant vectors, and methods of using FLAME-1 to identify substrates,
 CC activators or inhibitors of FLAME-1 are provided. FLAME-1, FLAME-2 (see
 CC AA90108) and agonists can be used to inhibit apoptosis, e.g. for
 CC treating HIV infection or Alzheimer's disease. Inhibitors can be used as
 CC apoptotic agents
 XX
 SQ Sequence 445 AA;

Query Match 96.7%; Score 504; DB 2; Length 445;
 Best Local Similarity 99.0%; Pred. No. 8.8e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDLIRRGKLSVGDLAELLY 63
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDLIRRGKLSVGDLAELLY 60
 QY 64 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
 DB 61 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 15
 AA26086
 ID AA26086 standard; protein; 445 AA.

AC AA26086;
 DT 14-NOV-2002 (first entry)
 XX Human FLAME-1 protein.

XX Human; FADD-like apoptotic/anti-apoptotic protein; Alzheimer's disease;
 KW gene therapy; human immunodeficiency virus; HIV infection; apoptosis;
 KW FLAME-1.
 XX Homo sapiens.

PH Key Location/Qualifiers
 FT Region 5..71
 FT /note= "FADD-DED-Homology A (FDH-A) region"
 FT Region 90..168
 FT /note= "FADD-DED-Homology B (FDH-B) region"
 FT Region 197..445
 FT /note= "Caspase-domain homology (CDH) region"
 FT Active-site 323..327
 FT Cleavage-site 338..342
 FT /note= "Caspase cleavage site"

XX US2002086983-A1.

PN 04-JUL-2002.

PD 22-AUG-2001; 2001US-00935223.

PF 28-OCT-1997; 97US-00959167.

XX 26-MAR-1999; 99US-00276993.

PR 28-NOV-2000; 2000US-00723450.

XX (UYJE-) UNIV JEFFERSON THOMAS.

PA Alnemri ES;

XX WPI; 2002-642259/69.

DR N-PSDB; AAD43202.

XX

PT Novel FADD-like apoptotic/anti-apoptotic proteins useful for inhibiting
 PT apoptosis, treating diseases characterized by apoptosis e.g. HIV
 PT infection and Alzheimer's disease, and for identifying modulators of the
 PT protein.

XX Claim 1; Page 14-15; 35pp; English.

XX The invention relates to FADD-like apoptotic/anti-apoptotic proteins
 CC (FLAME 1 or 2) and nucleic acid molecules encoding such proteins. FLAME
 CC sequences are useful for inhibiting apoptosis and for gene therapy of
 CC diseases characterised by apoptosis including HIV infection and
 CC Alzheimer's disease. FLAME inhibitors are useful as apoptotic agents and
 CC activators are useful as anti-apoptotic agents. FLAME-1 is useful as a
 CC substrate for caspase in assays to identify caspase inhibitors. The
 CC present sequence is human FLAME-1 protein

XX Sequence 445 AA;

Query Match 96.7%; Score 504; DB 5; Length 445;
 Best Local Similarity 99.0%; Pred. No. 8.8e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDLIRRGKLSVGDLAELLY 63
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDLIRRGKLSVGDLAELLY 60
 QY 64 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
 DB 61 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 16

AA67419

ID AAY67419 standard; protein; 462 AA.

XX AAY67419;

DT 12-MAY-2000 (first entry)

XX Usurpin-beta polypeptide.

XX Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;

KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;

KW caspase; cytostatic; antiParkinsonian; antidiabetic.

OS Homo sapiens.

XX WO200003023-A1.

XX 20-JAN-2000.

PF 07-JUL-1999; 99WO-CA000615.

XX 08-JUL-1998; 98US-0092005P.

XX (MERI) MERCK FROSST CANADA INC.

XX Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;

XX WPI; 2000-160929/14.

DR N-PSDB; AA256988.

XX Novel recombinant DNA molecules and polypeptides for treating apoptosis
 PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
 PT disease.

XX Claim 6; Fig 10B; 69pp; English.

XX The invention provides recombinant nucleic acid molecules encoding
 CC usurpin-alpha (lacking the first death effector domain (DED) or its
 CC prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are
 CC useful for in vitro and in vivo identification of usurpin-procaspase-8
 CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity

CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
 CC is useful for treating diseases like autoimmune diabetes, cancer and
 CC Parkinson's disease. Activators and inhibitors of usurin-procaspase-8
 CC interaction are also useful for treating various diseases mediated by
 CC apoptosis. Usurin provides an attractive model for modulating caspase
 CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be
 CC regulated at several levels in the presence of usurin, conferring
 CC resistance to Fas-ligand cell death. The present sequence represents the
 CC usurin-beta polypeptide
 XX
 SQ Sequence 462 AA;

Query Match 96.7%; Score 504; DB 3; Length 462;
 Best Local Similarity 99.0%; Pred. No. 9.2e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDIAELLY 63
 |||||
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDIAELLY 60
 |||||

QY 64 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
 |||||
 DB 61 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102
 |||||

RESULT 17
 ADR14101
 ID ADR14101 standard; protein; 462 AA.
 XX
 AC ADR14101;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human NF-kappaB pathway-associated protein SeqID102.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnary; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; human.
 XX
 XX Homo sapiens.
 OS
 XX WO2004065577-A2.
 PN
 XX
 XX 05-AUG-2004.
 XX
 XX 13-JAN-2004; 2004WO-US0000798.
 XX
 XX 14-JAN-2003; 2003US-0440068P.
 PR
 XX 12-MAY-2003; 2003US-0469757P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX Nadler SG, Neubauer MG, Feder JN, Carman J;
 PI WPI; 2004-562168/54.
 XX
 XX N-PSDB; ADR14100.
 DR
 XX New isolated polynucleotides and polypeptides associated with NF-kappaB
 XX pathway, useful for diagnosing, treating, or preventing disorders or
 PT

PT diseases associated with NF-kappaB pathway.
 XX
 XX Claim 6; SEQ ID NO 102; 237pp; English.
 XX
 CC This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
 CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnary activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory apoptosis,
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.
 XX
 SQ Sequence 462 AA;

Query Match 96.7%; Score 504; DB 8; Length 462;
 Best Local Similarity 99.0%; Pred. No. 9.2e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDIAELLY 63
 |||||
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDIAELLY 60
 |||||

QY 64 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
 |||||
 DB 61 RVRPDLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102
 |||||

RESULT 18
 AAW58578
 ID AAW58578 standard; protein; 480 AA.
 XX
 XX AAW58578;
 XX
 XX 07-SEP-1998 (first entry)
 DT
 XX Human FIN-1.
 DE
 XX Human; FIN-1; FLICE inhibitor-1; ICE-LAP7; death effector domain; DED;
 KW apoptosis-related protein; caspase; viral infection; cancer; tumour;
 KW diagnosis; ischaemic injury; neuro-degenerative disorder.
 XX
 XX Homo sapiens.
 OS
 XX EP841399-A2.
 PN
 XX 13-MAY-1998.
 PD
 XX 10-NOV-1997; 97EP-00309003.
 PF
 XX 12-NOV-1996; 96US-00748086.
 PR
 XX (SMIX) SMITHKLINE BEECHAM CORP.
 PA
 XX

PI Kikly K, Emery JG;
 XX WPI; 1998-252943/23.
 DR N-PSDB; AAV31375.
 XX
 PT New nucleic acid encoding human apoptosis-related protein - used for
 PT diagnosis and treatment of e.g. viral infections, tumour, ischaemic
 PT injury and neuro-degenerative disorders.
 XX
 PS Claim 11; Page 25-27; 48pp; English.
 XX
 CC The present sequence represents human FIN-1 (FLICE inhibitor-1), which is
 CC a caspase. FLICE (ICE-LAP7) is a protease of the interleukin-converting
 CC enzyme family, a protein involved in the regulation of cell death. A host
 CC cell, comprising a vector containing FIN-1 encoding DNA, can be used to
 CC produce FIN-1. The vector containing the DNA can be used for producing a
 CC cell which expresses a polypeptide by transforming or transfecting the
 CC cell with it so that the cell expresses the polypeptide encoded the human
 CC cDNA contained in the vector. The polypeptide or its antagonist can be
 CC used in the treatment of patients needing FIN-1 by in-vivo
 CC administration. Conditions which may be treated include viral infection,
 CC tumours (especially solid tumours), ischaemic injury (e.g. stroke or
 CC myocardial infarction), neurodegenerative disorders (e.g. Alzheimer's or
 CC Parkinson's disease), osteoporosis, osteoarthritis, polycystic kidney
 CC disease, chronic degenerative liver disease, acquired immunodeficiency
 CC syndrome (AIDS) and aplastic anaemia. The polynucleotides may also be
 CC used for chromosome identification
 XX
 SQ Sequence 480 AA;
 Query Match 96.7%; Score 504; DB 2; Length 480;
 Best Local Similarity 99.0%; Pred. No. 9.6e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLILRERKLSVGDLAELLY 63
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLILRERKLSVGDLAELLY 60
 QY 64 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
 DB 61 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
 RESULT 19
 AAW69715
 ID AAW69715 standard; protein; 480 AA.
 XX
 AC AAW69715;
 XX
 DT 24-NOV-1998 (first entry)
 XX
 DE Human Casper protein.
 XX
 KW Casper; caspase-eight-related protein; human; apoptosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9833883-A1.
 XX
 PD 06-AUG-1998.
 XX
 PF 05-FEB-1998; 98WO-US002117.
 XX
 PR 05-FEB-1997; 97US-00795088.
 XX
 PA (TULA-) TULARIK INC.
 XX
 PI Shu H, Goeddel DV;
 XX
 DR WPI; 1998-437440/37.
 DR N-PSDB; AAV50436.
 XX
 PT New Casper protein involved in regulation of apoptosis - used, e.g. to

PT identify specific modulators, identify or isolate similar sequences and
 PT in gene therapy.
 XX
 PS Claim 1; Page 22-23; 29pp; English.
 XX
 CC This is the amino acid sequence of a novel human protein, designated
 CC Casper (for caspase-eight-related protein), that is involved in
 CC regulation of apoptosis. The sequence is deduced from an isolated cDNA
 CC clone (see AAV50436). Casper protein interacts with FADD and is recruited
 CC to Fas. It also interacts with caspase-8 and caspase-3, and with TRAF1
 CC and TRAF2. A claimed isolated polypeptide comprises the full-length
 CC Casper amino acid sequence, or a fragment of at least 6 consecutive amino
 CC acid residues including at least one of residues 1-96, 1-202, 1-435, 78-
 CC 480, 192-480, 390-480 or residue 360. The isolated protein, or cells that
 CC express the protein, can be used to screen for agents, e.g. antibodies or
 CC T-cell receptors, that specifically modify the binding of Casper to a
 CC target, and thus its function
 XX
 SQ Sequence 480 AA;
 Query Match 96.7%; Score 504; DB 2; Length 480;
 Best Local Similarity 99.0%; Pred. No. 9.6e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLILRERKLSVGDLAELLY 63
 DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLILRERKLSVGDLAELLY 60
 QY 64 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
 DB 61 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
 RESULT 20
 AAW69229
 ID AAW69229 standard; protein; 480 AA.
 XX
 AC AAW69229;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE I-FLICE-1 protein.
 XX
 KW I-FLICE-1; FADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;
 KW CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;
 KW CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;
 KW multiple sclerosis; head injury; cancer; autoimmune disorder; therapy;
 KW viral infection; graft versus host disease; graft rejection.
 XX
 OS Homo sapiens.
 XX
 PN WO9831801-A1.
 XX
 PD 23-JUL-1998.
 XX
 PF 21-JAN-1998; 98WO-US000969.
 XX
 PR 21-JAN-1997; 97US-0034205P.
 PR 05-AUG-1997; 97US-0054800P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
 XX
 DR WPI; 1998-414100/35.
 DR N-PSDB; AAV44806.
 XX
 PT New inhibitory polypeptides of FLICE - used to develop products for
 PT treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis, cancers,
 PT autoimmune disorders, viral infection or graft rejection.
 XX
 PS Claim 9; Fig 1; 118pp; English.

XX This sequence is an inhibitor of Fas-ligand associated with death
 CC domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The
 CC proteins can inhibit both TNFR-1 and CD-95 induced apoptosis. These are
 CC the first examples of a naturally occurring catalytically inactive
 CC caspase that can act as a dominant negative inhibitor of apoptosis. The
 CC polypeptides and agonists can be used for treating e.g. Alzheimer's
 CC disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis,
 CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
 CC cell death associated with cardiovascular disease, polycystic kidney
 CC disease, apoptosis of endothelial cells in cardiovascular disease,
 CC degenerative liver disease, multiple sclerosis (MS) and head injury
 CC damage. Antagonists of the polypeptides can be used for treating cancers
 CC (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
 CC dependent tumours, and cancers of the breast, ovary, prostate, bone,
 CC liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
 CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
 CC arthritis), and viral infections (e.g. herpes viruses, pox viruses and
 CC adenoviruses), graft versus host disease, acute disease, acute graft
 CC rejection, and chronic graft rejection. The products can also be used for
 CC detection, diagnosis and drug screening
 XX
 SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 2; Length 480;
 Best Local Similarity 99.0%; Pred. No. 9.6e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNVRDLDIRRGKLSVGDIAELLY 63
 DB 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNVRDLDIRRGKLSVGDIAELLY 60
 QY 64 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIEIG 105
 DB 61 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 21
 AAW78903
 ID AAW78903 standard; protein; 480 AA.
 XX
 AC AAW78903;
 XX
 DT 11-JAN-1999 (first entry)
 DE Human G1 protein isoform alpha (CASH-alpha).
 XX
 KW G1 protein; CASH-alpha; human; caspase homologue; Fas receptor;
 KW modulator; apoptosis; cell death; inflammation; tumour; HIV; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 2..73
 FT /note= "death domain/MORT module"
 FT Domain 93..142
 FT /note= "death domain/MORT module"
 XX
 PN WO9839435-A1.
 XX
 PD 11-SEP-1998.
 XX
 PF 26-FEB-1998; 98WO-IL000098.
 XX
 PR 03-MAR-1997; 97IL-00120367.
 PR 01-MAY-1997; 97IL-00120759.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Wallach D, Goltsev Y, Kovalenko A, Varfolomeev E, Brodianski V;
 XX WPI; 1998-495842/42.
 DR N-PSDB; AAV52968.

XX New DNA encoding isoforms of G1 protein which bind MORT-1 - and regulate
 PT the effects of Fas and tumour necrosis factor receptors, useful for
 XX killing of cells e.g. HIV and cancer cells.
 PS Claim 12; Fig 1B; 132pp; English.
 XX
 CC This is the amino acid sequence of the alpha isoform of novel human G1
 CC protein. The sequence is deduced from an isolated skin fibroblast cDNA
 CC clone (see AAV52968). G1-alpha (also called CASH alpha, CASH being
 CC caspase homologue) and a shorter isoform, G1-beta (see AAW78904),
 CC represent 2 splice variants of the G1 protein. These G1 proteins are
 CC capable of binding to, or interacting directly or indirectly via their N
 CC terminal MORT modules, with MORT-1 or with MORT-binding proteins such as
 CC Mch4 (CASP-10) and MACH (CASP-8), and thereby of binding to the
 CC intracellular domain of the Fas-R receptor, to which MORT-1 binds, or of
 CC binding to the intracellular domain of the p55 tumour necrosis factor
 CC (TNF) receptor, to which TRADD binds and to which TRADD protein MORT-1
 CC binds. Hence, they are considered as mediators or modulators of Fas-R
 CC having a role in e.g. the signalling process that is initiated by the
 CC binding of Fas ligand to Fas-R, and also having a role in the signalling
 CC process initiated by the binding of TNF to p55-R. The longer isoform also
 CC has a C-terminal caspase activity region involved in cytotoxic activity.
 CC G1 DNA (I) and polypeptide (II), vectors and fragments are used to
 CC regulate cell death or inflammatory processes. (II) is used to inhibit
 CC cell death, and its inhibitors augment/enhance the processes. (I) and
 CC (II) regulate the Fas-R ligand or TNF effect on cells carrying an Fas-R
 CC or p55-R. Tumour, HIV-infected or other diseased cells can be treated
 CC using a viral vector encoding a viral surface protein, which binds a
 CC specific cell surface receptor and a sequence encoding (II), which kills
 CC the cell. Antisense oligonucleotides, introduced using the above vector,
 CC block the expression of (II) and can also regulate the above effects.
 CC These effects can also be regulated using a vector encoding a ribozyme
 CC that interacts with a cellular mRNA encoding (II), and allows (II)
 CC expression
 XX
 SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 2; Length 480;
 Best Local Similarity 99.0%; Pred. No. 9.6e-51;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNVRDLDIRRGKLSVGDIAELLY 63
 DB 1 MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNVRDLDIRRGKLSVGDIAELLY 60
 QY 64 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIEIG 105
 DB 61 RVRFPDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 22
 AAW76631
 ID AAW76631 standard; protein; 480 AA.
 XX
 AC AAW76631;
 XX
 DT 12-JUL-1999 (first entry)
 DE Human CFLIP-L protein.
 XX
 KW Death effector domain; human; murine; anti-apoptotic; treatment;
 KW HIV infection; autoimmune disease; FLIP protein.
 XX
 OS Homo sapiens.
 XX
 PN DE19713393-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 01-APR-1997; 97DE-01013393.
 XX
 PR 01-APR-1997; 97DE-01013393.

```

XX PA (TSCH/) TSCHOPP J.
XX PI Tschopp J, Thome M, Burns K, Irmeler M, Hahne M, Schroeter M;
XX PI Schneider P, Bodmer J, Steiner V, Rimoldi D, Hoffmann K, French EL;
XX DR WPI; 1998-532710/46.
XX DR N-PSDB; AAV61937.
XX PT New DNA encoding for anti-apoptotic gene product - used to treat HIV
XX PT infections and autoimmune diseases.
XX PS Claim 20; Fig 4B; 45pp; German.
XX CC This invention describes novel human and mouse anti-apoptotic gene
XX CC products which contain at least one death effector domain. The products
XX CC of the invention are used in the treatment of HIV infections and
XX CC autoimmune diseases
XX SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 2; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKGLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKGLSVGDLAELLY 60

QY 64 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
DB 61 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102

RESULT 23
AAV05787
ID AAY05787 standard; protein; 480 AA.
AC AAY05787;
XX 02-AUG-1999 (first entry)
DE Human MACH related inducer of toxicity MRIT alpha 1.
XX MRIT alpha 1; MACH related inducer of toxicity; human; apoptosis;
XX pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
XX atherosclerosis; neurodegenerative disease; Alzheimer's disease;
XX Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
XX aplastic anaemia; myocardial infarction; therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Region 1..165
FT /note= "death effector domain homology region"
FT Region 140..178
FT /note= "Bcl-2 homology region"
FT Region 136..228
FT /note= "Bcl-2 homology region"
FT Region 258..289
FT /note= "Bcl-2 homology region"
FT Region 299..350
FT /note= "Bcl-2 homology region"
FT Region 301..480
FT /note= "caspase homology region"
FT Region 356..397
FT /note= "Bcl-2 homology region"
FT Active-site 358..362
XX WO9918230-A2.
XX 15-APR-1999.
XX

```

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PF 07-OCT-1998; 98WO-US021132.
XX
PR 07-OCT-1997; 97US-00946226.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Chaudhary PM;
XX
XX WPI: 1999-277275/23.
XX DR N-PSDB; AAX25508.
XX
XX PT Identifying regulators of MACH-related inducer of toxicity.
XX
XX Example 1; Fig 1F; 78pp; English.
XX
XX The present sequence represents novel human MACH-related inducer of
XX toxicity (MRIT) isoform MRIT alpha 1, a CED-4 homologue that interacts
XX simultaneously with caspases and Bcl-2 family polypeptides, and which has
XX pro-apoptotic activity. Multiple isoforms of MRIT have been identified,
XX some of which function to induce caspase dependent apoptosis in mammalian
XX cells, e.g. MRIT alpha 1 and MRIT beta 1 (see AAY05789), while others
XX have anti-apoptotic activity, e.g. MRIT alpha 2 (see AAY05788). MRIT
XX alpha 1 includes an N-terminal death effector domain and a C-terminal
XX caspase homology domain, but is not a cysteine protease. Selective
XX enhancers and inhibitors of MRIT apoptotic activity can be identified and
XX used to treat diseases mediated by the dysfunction of programmed cell
XX death or proliferation. A cell accumulation disorder such as cancer,
XX autoimmune disease, viral infection, angiogenesis or atherosclerosis is
XX treated by administering an agent that selectively enhances MRIT
XX apoptotic activity, thereby inducing apoptosis in a subject. A disorder
XX of cell loss, such as a neurodegenerative disorder, including Alzheimer's
XX disease, Parkinson's disease, retinitis pigmentosa, stroke, aplastic
XX anaemia, myocardial infarction or AIDS can be treated by administering an
XX agent that selectively inhibits MRIT apoptotic activity
XX SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 2; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKGLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKGLSVGDLAELLY 60

QY 64 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
DB 61 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102

RESULT 24
AAY57454
ID AAY57454 standard; protein; 480 AA.
XX
XX AC AAY57454;
XX
XX DT 25-FEB-2000 (first entry)
XX
XX DE Human FLICE-like inhibitory protein long form protein sequence.
XX
XX KW Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;
XX KW FLICE-like inhibitory protein short form; apoptosis inhibitor;
XX KW atherosclerosis; vascular wall inflammation; vascular injury;
XX KW Fas ligand-mediated apoptosis; atherosclerosis; transplant.
XX
XX OS Homo sapiens.
XX
XX PN WO9942570-A1.
XX
XX PD 26-AUG-1999.
XX
XX PF 19-FEB-1999; 99WO-US003558.
XX

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```

PR 20-FEB-1998; 98US-0075471P.
XX
XX (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
XX
XX Walsh K;
XX
XX WPI; 1999-527469/44.
XX
XX N-PSDB; AA239040.
XX
XX Treating conditions characterized by vascular wall inflammation.
XX
XX Claim 5; Page 69-71; 105pp; English.
XX
XX The present sequence represents human FLICE-like inhibitory protein long
XX form, designated FIP-L. The present invention describes a new treatment
XX of a condition characterised by vascular wall inflammation in a subject
XX comprising administering a FIP molecule to inhibit Fas ligand-mediated
XX apoptosis of vascular endothelial cells in the subject. The method can be
XX used to treat atherosclerosis, transplant arteriosclerosis and vascular
XX injury
XX
XX Sequence 480 AA;
XX
XX Query Match 96.7%; Score 504; DB 2; Length 480;
XX Best Local Similarity 99.0%; Pred. No. 9.6e-51;
XX Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDLAELLY 60
QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 25
AA57606
ID RAY59414 standard; protein; 480 AA.
XX
XX AA57606;
XX
XX 21-MAR-2000 (first entry)
XX
XX Human CLARP protein sequence.
XX
XX RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;
XX caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;
XX CIDE-A; CIDE-B; DRP-1; diagnosis; cell growth; apoptosis dysregulation;
XX gene therapy; cardiac disorder; cancer; neurodegenerative disease; AIDS;
XX aplastic anaemia; ischaemic injury; toxin-induced liver disease; CLARP.
XX
XX Homo sapiens.
XX
XX WO955134-A2.
XX
XX 04-NOV-1999.
XX
XX 27-APR-1999; 99WO-US009183.
XX
XX 27-APR-1998; 98US-00069023.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Nunez G, Inohara N, Koseki T;
XX
XX WPI; 2000-072163/06.
XX
XX N-PSDB; AA248769.
XX
XX Compositions for identifying apoptosis signalling pathway inhibitors
XX useful for treating diseases.
XX
XX Example 10; Fig 21b; 93pp; English.
XX

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```

XX
XX This sequence is the human CLARP protein. The invention relates to the
XX human RICK (RIP-like interacting CLARP kinase) protein. The RICK protein
XX acts as a positive regulator of apoptosis, potentiating apoptosis induced
XX by caspase-8 and caspase-10 during CD95 signalling. The invention
XX provides methods for identifying apoptosis signalling pathway inhibitors
XX and activators, and methods and compositions for screening compounds
XX which will modulate the interactions of the various compositions
XX identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B
XX and DRP-1). RICK is useful in screening assays for agents, useful in the
XX diagnosis, prognosis or treatment of disease associated with excess cell
XX growth and dysregulation of apoptosis. Complexes containing RICK and
XX CLARP can be used in drug screening assays to identify inhibitor
XX molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an
XX in vitro cell system can be used to identify inhibitors of the enzymatic
XX activity of caspase-8. Identification of ARC-like inhibitory compounds
XX may be useful for gene therapy treatment of disease with increased cell
XX death in muscle tissue and cardiac disorders. Therapeutic compositions of
XX CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative
XX disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver
XX disease. AntiRICK antibodies can be used as reagents for the preparation
XX or affinity chromatography media, and for diagnostically measuring RICK
XX levels. A specific inhibitor of an essential step in the biochemistry of
XX apoptosis is needed. RICK interaction with intracellular factors such as
XX CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK
XX binding to intracellular apoptosis factors are potential drug candidates
XX
XX Sequence 480 AA;
XX
XX Query Match 96.7%; Score 504; DB 3; Length 480;
XX Best Local Similarity 99.0%; Pred. No. 9.6e-51;
XX Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDLAELLY 60
QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 26
AA57606
ID AAY57606 standard; protein; 480 AA.
XX
XX AAY57606;
XX
XX 10-MAR-2000 (first entry)
XX
XX Human apoptosis associated protein HAPOP-1.
XX
XX Human; apoptosis associated protein; HAPOP; diagnosis; cytostatic;
XX antiarteriosclerotic; antiarthritic; hepatotropic; apoptosis regulator;
XX cell proliferative disorder; atherosclerosis; arteriosclerosis; cancer;
XX immune disorder; rheumatoid arthritis; systemic lupus erythematosus;
XX reproductive disorder; tumour; gastrointestinal disorder; cirrhosis;
XX colitis; hepatitis; pancreatitis.
XX
XX Homo sapiens.
XX
XX WO9958692-A2.
XX
XX 18-NOV-1999.
XX
XX 11-MAY-1999; 99WO-US010386.
XX
XX 13-MAY-1998; 98US-00078402.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Hillman JL, Corley NC, Guegler KJ, Patterson C, Baughn M;
XX

```

DR WPI: 2000-062303/05.
 DR N-PSDB; AA247926.
 XX
 PT New protein for diagnosing, treating or preventing disorders associated
 PT with increased or decreased apoptosis.
 XX
 PS Claim 1; Page 70-71; 81pp; English.
 XX
 CC The present sequence represents a human apoptosis associated protein
 CC designated HAPOP-1. HAPOP proteins are apoptosis regulators which have
 CC antiarteriosclerotic, cytoskeletal, antiarthritic and hepatotropic
 CC activity. A pharmaceutical composition comprising HAPOP in conjunction
 CC with a carrier, a purified antagonist of HAPOP, vectors and agonists of
 CC HAPOP, are administered for diagnosing, treating or preventing disorders
 CC associated with increased or decreased apoptosis, e.g. cell proliferative
 CC disorders such as atherosclerosis, arteriosclerosis and cancers; immune
 CC disorders such as rheumatoid arthritis, systemic lupus erythematosus;
 CC reproductive disorders such as prostate cancer, endometrial and ovarian
 CC tumours; and gastrointestinal disorders such as cirrhosis, colitis,
 CC hepatitis and pancreatitis. The polynucleotides encoding HAPOP proteins
 CC may be useful to detect and quantitate expression of HAPOP genes which
 CC are correlated with diseases and are also useful to detect differences in
 CC the chromosomal location due to translocation, inversion etc., among
 CC normal, carrier, or affected individuals. The combination of the
 CC therapeutic agents may act synergistically to effect the treatment or
 CC prevention of various disorders providing improved efficacy with lower
 CC dosages of each agent and thus reducing the potential for adverse side
 CC effects
 XX
 SQ Sequence 480 AA;
 Query Match 96.7%; Score 504; DB 3; Length 480;
 Best Local Similarity 99.0%; Pred. No. 9.6e-51; Indels 0; Gaps 0;
 Matches 101; Conservative 1; Mismatches 0;
 QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDIAELLY 63
 Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDIAELLY 60
 QY 64 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
 Db 61 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102
 RESULT 27
 AA167418
 ID AAY67418 standard; protein; 480 AA.
 XX
 AC AAY67418;
 XX
 DT 12-MAY-2000 (first entry)
 XX
 DE Usurpin-alpha polypeptide.
 XX
 KW Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;
 KW usurpin-gamma; procaspase-8; CP95; apoptosis; cancer; immunosuppressive;
 KW caspase; cytoskeletal; antiParkinsonian; antidiabetic.
 XX
 OS Homo sapiens.
 XX
 PN WO200003023-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 07-JUL-1999; 99WO-CA000615.
 XX
 PR 08-JUL-1998; 98US-0092005P.
 XX
 PA (MERI) MERCK FROST CANADA INC.
 XX
 PI Nicholson DM, Rasper DM, Xanthoudakis S, Roy S;
 XX
 DR WPI: 2000-160929/14.

DR N-PSDB; AA256987.
 XX
 PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
 PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
 XX
 PS Claim 6; Fig 9B; 69pp; English.
 XX
 CC The invention provides recombinant nucleic acid molecules encoding
 CC usurpin-alpha (lacking the first death effector domain (DED) or its
 CC prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are
 CC useful for in vitro and in vivo identification of usurpin-procaspase-8
 CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity
 CC of cells to CP95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
 CC is useful for treating diseases like autoimmune diabetes, cancer and
 CC Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8
 CC interaction are also useful for treating various diseases mediated by
 CC apoptosis. Usurpin provides an attractive model for modulating caspase
 CC activation. Sensitivity of cells bearing CP95(Fas/Apo-1) receptor can be
 CC regulated at several levels in the presence of usurpin, conferring
 CC resistance to Fas-ligand cell death. The present sequence represents the
 CC usurpin-alpha polypeptide
 XX
 SQ Sequence 480 AA;
 Query Match 96.7%; Score 504; DB 3; Length 480;
 Best Local Similarity 99.0%; Pred. No. 9.6e-51; Indels 0; Gaps 0;
 Matches 101; Conservative 1; Mismatches 0;
 QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDIAELLY 63
 Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGDIAELLY 60
 QY 64 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
 Db 61 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102
 RESULT 28
 AAB03960
 ID AAB03960 standard; protein; 480 AA.
 XX
 AC AAB03960;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE FLICE-like inhibitor protein (Genbank Accession No. 2253679).
 XX
 KW Chimeric protein; fusion protein; FLICE like inhibitor protein; FLIP;
 KW Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
 KW tumour specific antigen; immune response; therapy; prophylaxis;
 KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;
 KW acquired immune deficiency syndrome; human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2000059935-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 05-APR-2000; 2000WO-US009002.
 XX
 PR 05-APR-1999; 99US-0127867P.
 XX
 PR 06-APR-1999; 99US-0128021P.
 XX
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 PA (PAYA/) PAYA C.
 PA (ALGE/) ALGECIRAS-SCHMINICH A.
 XX
 PI Paya C, Algeciras-Schminich A;
 XX
 DR WPI: 2000-664988/64.

XX Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
PT comprises portion of anti-apoptotic polypeptide linked to a transport
PT group.
XX
XX Disclosure; Page 79-81; 89pp; English.
XX
XX A chimeric group or fusion peptide which comprises a portion of an anti-
CC apoptotic polypeptide which inhibits apoptosis of lymphocytes in
CC combination with a transport group is described. The transport group is
CC capable of transporting the chimeric group or fusion peptide across the
CC cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor
CC protein (FLIP) which inhibits Fas and TNF mediated apoptosis by
CC inhibiting binding of Caspase-8 to the Fas receptor complex, thus
CC shutting off the downstream Fas signalling pathway. The chimeric group
CC and fusion peptide are useful for inhibiting ligand-induced apoptosis by
CC bringing them into contact with T cells. The chimeric group is useful for
CC expanding T cells in vitro e.g. T cells specific for particular antigens
CC such as tumour-specific antigen, for enhancing immune response and to
CC inhibit the apoptosis of chronically activated T cells e.g. activated
CC CD4⁺ T cells in HIV infected patients. The chimeric group is also useful
CC for therapeutic, prophylactic or diagnosis of intracellular delivery of
CC small molecules and macromolecules such as anti-apoptotic polypeptides
CC and nucleic acids encoding such polypeptides
XX
XX Sequence 480 AA;
SQ

Query Match 96.7%; Score 504; DB 3; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDLAELLY 60
QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 29
ABB09294
ID ABB09294 standard; protein; 480 AA.
XX
XX ABB09294;
XX
XX
DT 15-JUL-2002 (first entry)
XX
DE Human FLIP-c protein SEQ ID NO:11.
XX
XX Human; FLIP-c; caspase 8 dominant negative regulator; antiinflammatory;
XX anti-tumour; FLIP-c inhibitor; apoptosis; antisense gene therapy;
XX phosphorothioate; antisense modulation; infection; inflammation; tumour.
XX
OS Homo sapiens.
XX
XX WO200224717-A1.
XX
XX
PD 28-MAR-2002.
XX
XX 14-SEP-2001; 2001WO-US028732.
XX
XX 20-SEP-2000; 2000US-00666269.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ackermann EU, Bennett CF, Zhang H, Watt AT, Ricketts W, Dean NM;
XX WPI; 2002-404948/43.
XX N-PSDB; ABL52333.
XX
XX Novel antisense compound that hybridizes and inhibits nucleic acid
PT encoding a natural dominant negative regulator of caspase 8, FLIP-c,

PT useful for preventing or delaying infection, inflammation or tumor
PT formation.
XX
XX Example 13; Page 118-120; 154pp; English.
XX
XX The present invention describes a compound (I) 8-50 nucleobases in length
CC targeted to a nucleic acid molecule (II) encoding a natural dominant
CC negative regulator of caspase 8, FLIP-c, where (I) specifically
CC hybridises with and inhibits expression of the protein, or specifically
CC hybridises with at least an 8-nucleobase portion of an active site on
CC (II). (I) has antiinflammatory and anti-tumour activities. (I) is an
CC inhibitor of FLIP-c expression, a modulator of apoptosis and can be used
CC in antisense gene therapy. (I) is useful for inhibiting the expression of
CC FLIP-c in cells or tissues, and for treating an animal having a disease
CC or condition associated with FLIP-c. (I) is also useful for modulating
CC apoptosis in a cell, where a caspase such as caspase 8, caspase 3 or
CC caspase 7 is activated, and the FLIP-c is the long form of FLIP-c. (I) is
CC also useful for diagnostics, therapeutics, prophylaxis, as research
CC reagents and kits, for distinguishing functions of various members of a
CC biological pathway, and in antisense gene therapy. (I) is also useful
CC prophylactically, e.g., to prevent or delay infection, inflammation or
CC tumour formation. The present sequence represents human FLIP-c as given
XX in an example from the present invention
XX
XX Sequence 480 AA;
SQ

Query Match 96.7%; Score 504; DB 5; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDLAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDLAELLY 60
QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
DB 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 30
ADA10615
ID ADA10615 standard; protein; 480 AA.
XX
XX ADA10615;
XX
XX 06-NOV-2003 (first entry)
XX
DE Human inhibitor of FLICE (I-FLICE-1) protein.
XX
XX Human; I-FLICE-1; inhibitor of FLICE; FADD-like ICE;
XX tumour necrosis factor receptor-1 inhibitor; TNFR-1 inhibitor;
XX CD-95 induced apoptosis; apoptosis associated disease;
XX Alzheimer's disease; rheumatoid arthritis; stroke; osteoporosis;
XX ischaemia; septic shock; degenerative liver disease;
XX cardiovascular disorder; aberrant cell survival; neurotropic;
XX antirheumatic; vasotrophic; hepatotropic; osteopathic; cardiac;
XX cerebroprotective; antibacterial; antiarthritic; vasodilator.
XX
OS Homo sapiens.
XX
XX US2003087339-A1.
XX
XX 08-MAY-2003.
XX
XX 21-JAN-1998; 98US-00009893.
XX
XX 21-JAN-1997; 97US-0034205P.
XX 05-AUG-1997; 97US-0054800P.
XX
XX (NIJG/) NI J.
XX (ROSE/) ROSEN C A.
XX (DIXI/) DIXIT V M.
XX (GENT/) GENTZ R L.

PA (KENN/) KENNY J J.
XX
PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
XX
DR WPI; 2003-576674/54.
DR N-PSDB; ADA10614.
XX
XX New I-FLICE-1 (inhibitor of FLICE 1) or I-FLICE-2 nucleic acids, useful
PT for treating diseases associated with apoptosis e.g., Alzheimer's
PT disease, rheumatoid arthritis, stroke, osteoporosis, ischemia or septic
PT shock.
XX
XX Claim 1; Fig 1A-1B; 48pp; English.
PS
XX The present invention relates to the isolation of novel human I-FLICE-1
XX (inhibitor of FLICE (FADD-like ICE)) and I-FLICE-2 proteins, and the
CC polynucleotide sequences encoding them. The I-FLICE-1 and I-FLICE-2
CC proteins are novel inhibitors of tumour necrosis factor receptor-1 (TNFR-
CC 1) and CD-95 induced apoptosis. Also disclosed are vectors, host cells
CC and recombinant methods for producing the I-FLICE proteins. The sequences
CC and methods are useful for treating diseases associated with apoptosis
CC e.g. Alzheimer's disease, rheumatoid arthritis, stroke, osteoporosis,
CC ischaemia, septic shock, degenerative liver disease, and cardiovascular
CC disorders. They are also useful for diagnosing diseases or disorders
CC associated with aberrant cell survival in an individual. The present
CC sequence represents human I-FLICE-1.
XX
SQ Sequence 480 AA;

Query Match 96.7%; Score 504; DB 7; Length 480;
Best Local Similarity 99.0%; Pred. No. 9.6e-51;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDTLRERKLSVGDIAELLY 63
DB 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDTLRERKLSVGDIAELLY 60

QY 64 RVRFRDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
DB 61 RVRFRDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 102

Search completed: September 30, 2005, 08:00:06
Job time : 74 secs

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OM protein - protein search, using sw model

Run on: September 30, 2005, 07:58:49 ; Search time 1888 Seconds
(without alignments)
23.086 Million cell updates/sec

Title: US-09-402-569-2
Perfect score: 521
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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Database : Published Applications AA.*

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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	504	96.7	221	9 US-09-410-194-15	Sequence 15, Appl
2	504	96.7	221	9 US-09-410-194-22	Sequence 22, Appl
3	504	96.7	221	16 US-10-849-901-4	Sequence 4, Appl
4	504	96.7	221	17 US-10-832-218-15	Sequence 15, Appl
5	504	96.7	221	17 US-10-832-218-22	Sequence 22, Appl
6	504	96.7	221	18 US-10-998-582-4	Sequence 4, Appl
7	504	96.7	445	9 US-09-935-223-2	Sequence 2, Appl
8	504	96.7	445	16 US-10-825-282-44	Sequence 44, Appl
9	504	96.7	462	16 US-10-755-889-102	Sequence 102, Appl
10	504	96.7	480	9 US-09-861-270-2	Sequence 2, Appl
11	504	96.7	480	9 US-09-410-194-11	Sequence 11, Appl

Query Match 96.7% ; Score 504 ; DB 9 ; Length 221 ;

12 504 96.7 480 9 US-09-410-194-17 Sequence 17, Appl

13 504 96.7 480 10 US-09-009-893-2 Sequence 2, Appl

14 504 96.7 480 10 US-09-471-749-1 Sequence 1, Appl

15 504 96.7 480 16 US-10-408-765A-275 Sequence 275, App

16 504 96.7 480 16 US-10-713-208-2 Sequence 2, Appl

17 504 96.7 480 16 US-10-849-901-2 Sequence 2, Appl

18 504 96.7 480 17 US-10-832-218-11 Sequence 11, Appl

19 504 96.7 480 17 US-10-832-218-17 Sequence 17, Appl

20 504 96.7 480 18 US-10-998-582-2 Sequence 2, Appl

21 465 89.3 93 9 US-09-864-761-36370 Sequence 36370, A

22 390 74.9 481 9 US-09-410-194-12 Sequence 12, Appl

23 390 74.9 481 9 US-09-410-194-19 Sequence 19, Appl

24 390 74.9 481 17 US-10-832-218-12 Sequence 12, Appl

25 390 74.9 481 17 US-10-832-218-19 Sequence 19, Appl

26 390 74.9 484 13 US-10-005-921-2 Sequence 2, Appl

27 390 74.9 484 16 US-10-849-901-5 Sequence 5, Appl

28 390 74.9 484 18 US-10-998-582-5 Sequence 5, Appl

29 129.5 24.9 169 9 US-09-410-194-2 Sequence 2, Appl

30 129.5 24.9 169 17 US-10-832-218-2 Sequence 2, Appl

31 129.5 24.9 188 9 US-09-410-194-23 Sequence 23, Appl

32 129.5 24.9 188 17 US-10-832-218-23 Sequence 23, Appl

33 121.5 23.3 169 9 US-09-410-194-5 Sequence 5, Appl

34 121.5 23.3 169 17 US-10-832-218-5 Sequence 5, Appl

35 119 22.8 165 9 US-09-410-194-6 Sequence 6, Appl

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37 114.5 22.0 482 18 US-10-627-556-458 Sequence 458, App

38 114.5 22.0 977 18 US-10-627-556-494 Sequence 494, App

39 114.5 22.0 977 18 US-10-627-556-496 Sequence 496, App

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41 114.5 22.0 990 18 US-10-627-556-462 Sequence 462, App

42 105.5 20.2 171 9 US-09-410-194-4 Sequence 4, Appl

43 105.5 20.2 171 17 US-10-832-218-4 Sequence 4, Appl

44 105.5 20.2 182 9 US-09-410-194-24 Sequence 24, Appl

45 105.5 20.2 182 17 US-10-832-218-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-410-194-15

Sequence 15, Application US/09410194

Patent No. US20020095030A1

GENERAL INFORMATION:

APPLICANT: Tschopp, Margot

APPLICANT: Thome, Margot

APPLICANT: Burns, Kimberly

APPLICANT: Irmiler, Marten

APPLICANT: Hahne, Michael

APPLICANT: Schroter, Michael

APPLICANT: Schneider, Pascal

APPLICANT: Bodmer, Jean- Luc

APPLICANT: Steiner, Veronique

APPLICANT: Rimoldi, Donata

APPLICANT: Hofmann, Kay

APPLICANT: French, E. Lars

TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS

FILE REFERENCE: 11141-002001

CURRENT APPLICATION NUMBER: US/09/410,194

CURRENT FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: PCT/EP98/01857

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2

PRIOR FILING DATE: 1997-04-01

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 15

LENGTH: 221

TYPE: PRT

ORGANISM: Homo sapiens

US-09-410-194-15

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; Best Local Similarity 99.0%; Pred. No. 1.6e-47;
; Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDTLRLRERKLSVGDIAELLY 60

QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102

RESULT 2
US-09-410-194-22
; Sequence 22, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-22

Query Match 96.7%; Score 504; DB 9; Length 221;
Best Local Similarity 99.0%; Pred. No. 1.6e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102

RESULT 3
US-10-849-901-4
; Sequence 4, Application US/10849901
; Publication No. US20040230039A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: GOLTSEV, Yura
; APPLICANT: KOVALENKO, Andrei
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BRODIANSKI, Vadim
; TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
; FILE REFERENCE: WALLACH-23
; CURRENT APPLICATION NUMBER: US/10/849, 901
; CURRENT FILING DATE: 2004-05-21

; PRIOR APPLICATION NUMBER: US/09/380,546
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/IL98/00098
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: IL 120367
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: IL120759
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-849-901-4

Query Match 96.7%; Score 504; DB 16; Length 221;
Best Local Similarity 99.0%; Pred. No. 1.6e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102

RESULT 4
US-10-832-218-15
; Sequence 15, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/10/832,218
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-832-218-15

Query Match 96.7%; Score 504; DB 17; Length 221;
Best Local Similarity 99.0%; Pred. No. 1.6e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
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RESULT 5
US-10-832-218-22
; Sequence 22, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imtler, Marten
; APPLICANT: Hanne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/10/832,218
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-832-218-22

Query Match 96.7%; Score 504; DB 17; Length 221;
Best Local Similarity 99.0%; Pred. No. 1.6e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDILRERKLSVGDIAELLY 60

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Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
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RESULT 6
US-10-998-582-4
; Sequence 4, Application US/10998582
; Publication No. US20050152877A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: GOLTSEV, Yura
; APPLICANT: KOVALENKO, Andrei
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BRODIANSKI, Vadim
; TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; FILE REFERENCE: WALLACH-23
; CURRENT APPLICATION NUMBER: US/10/998,582
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US/09/380,546
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/IL98/00098
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: IL 120367
; PRIOR FILING DATE: 1997-03-03

; PRIOR APPLICATION NUMBER: IL120759
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-998-582-4

Query Match 96.7%; Score 504; DB 18; Length 221;
Best Local Similarity 99.0%; Pred. No. 1.6e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDILRERKLSVGDIAELLY 60

Qy 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
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RESULT 7
US-09-935-223-2
; Sequence 2, Application US/09935223
; Publication No. US20020086983A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, And
; TITLE OF INVENTION: Compositions For And Methods Of Making The Same
; FILE REFERENCE: TJU2499
; CURRENT APPLICATION NUMBER: US/09/935,223
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 09/723,450
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel Sequence
US-09-935-223-2

Query Match 96.7%; Score 504; DB 9; Length 445;
Best Local Similarity 99.0%; Pred. No. 3.7e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDILRERKLSVGDIAELLY 63
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDILRERKLSVGDIAELLY 60

Qy 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIGE 105
Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102
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RESULT 8
US-10-825-282-44
; Sequence 44, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282

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; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-282-44

Query Match          96.7%; Score 504; DB 16; Length 445;
Best Local Similarity 99.0%; Pred. No. 3.7e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKMLFLCRDVAIDVVPVPPNVRDLDLRLRERKGLSVGDLAELLY 63
Db 1 MSAEVIHQVEEALDTDEKMLFLCRDVAIDVVPVPPNVRDLDLRLRERKGLSVGDLAELLY 60

QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 9
US-10-755-889-102
; Sequence 102, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-102

Query Match          96.7%; Score 504; DB 16; Length 462;
Best Local Similarity 99.0%; Pred. No. 3.9e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKMLFLCRDVAIDVVPVPPNVRDLDLRLRERKGLSVGDLAELLY 63
Db 1 MSAEVIHQVEEALDTDEKMLFLCRDVAIDVVPVPPNVRDLDLRLRERKGLSVGDLAELLY 60

QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 10
US-09-861-270-2
; Sequence 2, Application US/09861270
; Patent No. US20020052474A1
; GENERAL INFORMATION:
; APPLICANT: Sul, Hong-Bing
; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/861,270
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,088
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-861-270-2

Query Match          96.7%; Score 504; DB 9; Length 480;
Best Local Similarity 99.0%; Pred. No. 4.1e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKMLFLCRDVAIDVVPVPPNVRDLDLRLRERKGLSVGDLAELLY 63
Db 1 MSAEVIHQVEEALDTDEKMLFLCRDVAIDVVPVPPNVRDLDLRLRERKGLSVGDLAELLY 60

QY 64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
Db 61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 11
US-09-410-194-11
; Sequence 11, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
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; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-11

Query Match          96.7%; Score 504; DB 9; Length 480;
Best Local Similarity 99.0%; Pred. No. 4.le-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPNVRDLDIRRGKLSVGDLAELLY 63
DB      1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPNVRDLDIRRGKLSVGDLAELLY 60

QY      64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
DB      61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 12
US-09-410-194-17
; Sequence 17, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Immler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-17

Query Match          96.7%; Score 504; DB 9; Length 480;
Best Local Similarity 99.0%; Pred. No. 4.le-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPNVRDLDIRRGKLSVGDLAELLY 63
DB      1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPNVRDLDIRRGKLSVGDLAELLY 60

QY      64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
DB      61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 13
US-09-009-893-2
; Sequence 2, Application US/09009893
; Publication No. US20030087339A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: GENTZ, REINER L.
; APPLICANT: KENNY, JOSEPH J.
; TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,893
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,800
; FILING DATE: 05-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0970002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-009-893-2

Query Match          96.7%; Score 504; DB 10; Length 480;
Best Local Similarity 99.0%; Pred. No. 4.le-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPNVRDLDIRRGKLSVGDLAELLY 63
DB      1 MSAEVIHQVEALDTDEKMLFLCRDVAIDVVPNVRDLDIRRGKLSVGDLAELLY 60

QY      64 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
DB      61 RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMAEIGE 102

RESULT 14
US-09-471-749-1
; Sequence 1, Application US/09471749
; Publication No. US20030124113A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS
```

/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Dr.
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/471,749
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/078,402
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Carrone, Michael C.
/ REGISTRATION NUMBER: 39,132
/ REFERENCE/DOCKET NUMBER: PF-0519 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 480 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: THPLBL02
/ CLONE: 157658
/ US-09-471-749-1

Query Match 96.7%; Score 504; DB 10; Length 480;
Best Local Similarity 99.0%; Pred. No. 4.1e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLILRERKLSVGDIAELLY 63
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLILRERKLSVGDIAELLY 60

QY 64 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
Db 61 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 102

RESULT 15
US-10-408-765A-275
/ Sequence 275, Application US/10408765A
/ Publication No. US20040101874A1
/ GENERAL INFORMATION:
/ APPLICANT: Ghosh, Soumitra S.
/ APPLICANT: Fahy, Eoin D.
/ APPLICANT: Zhang, Bing
/ APPLICANT: Gibson, Bradford W.
/ APPLICANT: Taylor, Steven W.
/ APPLICANT: Glenn, Gary M.
/ APPLICANT: Warnock, Dale E.
/ TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
/ FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
/ CURRENT APPLICATION NUMBER: US/10/408, 765A
/ CURRENT FILING DATE: 2003-04-04
/ NUMBER OF SEQ ID NOS: 3077
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 275
/ LENGTH: 480
/ TYPE: PRT
/ ORGANISM: Homo sapiens

US-10-408-765A-275

Query Match 96.7%; Score 504; DB 16; Length 480;
Best Local Similarity 99.0%; Pred. No. 4.1e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLILRERKLSVGDIAELLY 63
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLILRERKLSVGDIAELLY 60

QY 64 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
Db 61 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 102

RESULT 16
US-10-713-208-2
/ Sequence 2, Application US/10713208
/ Publication No. US20040121387A1
/ GENERAL INFORMATION:
/ APPLICANT: Ni et al.
/ TITLE OF INVENTION: I-PLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 and
/ TITLE OF INVENTION: CD-95 Induced Apoptosis
/ FILE REFERENCE: PF381C1D1
/ CURRENT APPLICATION NUMBER: US/10/713,208
/ PRIOR FILING DATE: 2003-11-17
/ PRIOR APPLICATION NUMBER: US 09/489,155
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US 09/009,893
/ PRIOR FILING DATE: 1998-01-21
/ PRIOR APPLICATION NUMBER: US 60/054,800
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: US 60/034,205
/ PRIOR FILING DATE: 1997-01-21
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 2
/ LENGTH: 480
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-713-208-2

Query Match 96.7%; Score 504; DB 16; Length 480;
Best Local Similarity 99.0%; Pred. No. 4.1e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLILRERKLSVGDIAELLY 63
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVPPNVRDLILRERKLSVGDIAELLY 60

QY 64 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 105
Db 61 RVRREFLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGE 102

RESULT 17
US-10-849-901-2
/ Sequence 2, Application US/10849901
/ Publication No. US20040230039A1
/ GENERAL INFORMATION:
/ APPLICANT: WALLACH, David
/ APPLICANT: GOLTSEV, Yura
/ APPLICANT: KOVALENKO, Andrei
/ APPLICANT: VARFOLOMEEV, Eugene
/ APPLICANT: BRODIANSKI, Vadim
/ TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
/ TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
/ FILE REFERENCE: WALLACH-23
/ CURRENT APPLICATION NUMBER: US/10/849,901
/ CURRENT FILING DATE: 2004-05-21
/ PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/380,546
/ PRIOR FILING DATE: CURRENT FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/IL98/00098

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; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: IL 120367
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: IL120759
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-849-901-2

Query Match          96.7%; Score 504; DB 16; Length 480;
Best Local Similarity 99.0%; Pred. No. 4.le-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4  MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 63
Db      1  MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 60

QY      64  RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
Db      61  RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102

RESULT 18
US-10-832-218-11
; Sequence 11, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/10/832,218
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-832-218-17

Query Match          96.7%; Score 504; DB 17; Length 480;
Best Local Similarity 99.0%; Pred. No. 4.le-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4  MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 63
Db      1  MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 60

QY      64  RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
Db      61  RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102

RESULT 19
US-10-832-218-17
; Sequence 17, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/10/832,218
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-832-218-17

Query Match          96.7%; Score 504; DB 17; Length 480;
Best Local Similarity 99.0%; Pred. No. 4.le-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4  MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 63
Db      1  MSAEVIHQVEALDTDEKEMLLFLCRDVAIDVVPNNVRLDILRERKLSVGDIAELLY 60

QY      64  RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
Db      61  RVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102

RESULT 20
US-10-998-582-2
; Sequence 2, Application US/10998582
; Publication No. US20050152877A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: GOLTSSEV, Yura
; APPLICANT: KOVALENKO, Andrei
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BRODIANSKI, Vadim
; TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; FILE REFERENCE: WALLACH=23
; CURRENT APPLICATION NUMBER: US/10/998,582
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US/09/380,546
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/IL98/00098
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: IL 120367
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: IL120759
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 20
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-998-582-2

Query Match          96.7%; Score 504; DB 18; Length 480;
Best Local Similarity 99.0%; Pred. No. 4.1e-47;
Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDIRRERKLSVGDIAELLY 63
   |||||
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDIRRERKLSVGDIAELLY 60
   |||||

QY 64 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
   |||||
Db 61 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102
   |||||

RESULT 21
US-09-864-761-36370
; Sequence 36370, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36370
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; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007272.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
; OTHER INFORMATION: SWISSPROT HIT: Q66674, EVALUAE 3.00e-04
; OTHER INFORMATION: EST_HUMAN HIT: W23795.1, EVALUAE 2.00e-46
US-09-864-761-36370

Query Match          89.3%; Score 465; DB 9; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.2e-43;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDIRRERKLSVGDIAELLY 63
   |||||
Db 1 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDIRRERKLSVGDIAELLY 60
   |||||

QY 64 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDY 96
   |||||
Db 61 RVRFDLLKRILKMDRKAVETHLLRNPHLVSDY 93
   |||||

RESULT 22
US-09-410-194-12
; Sequence 12, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschoopp, Jurq
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmier, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-410-194-12

Query Match          74.9%; Score 390; DB 9; Length 481;
Best Local Similarity 75.2%; Pred. No. 1.7e-34;
Matches 79; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPNNVRDLDIRRERKLSVGDIAE 60
   :|||
Db 3 QSPVSAEVIHQVEEALDTDEKEMLLFLCRDVTENLAAPNNVRDLDSLRSRGQLSFATLAE 62
   :|||
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Qy	61	LLYRVRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE	105
Db	63	LLYRVRFDLLKRILKTDKATVEDHLERNPHLVSDYRVLMSEIGE	107

RESULT 23

US-09-410-194-19
; Sequence 19, Application US/09410194
; Patent No. US2020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot

```

; APPLICANT: Imler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-02-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-410-194-19

```

	Query Match	74.9%;	Score 390;	DB 9;	Length 481;
	Best Local Similarity	75.2%;	Pred. No. 1.7e-34;		
	Matches	79;	Conservative	8;	Mismatches 18; Indels 0; Gaps 0;
Qy	1	KSRMSAEVHQHVEBALTDDEKEMLLFCRDVAIDVPPNVRDLDDIIRERKLSVGDLAE	60		
Dd	3	QSPSAEVIHQHVEECLEDEKEMLLFCRDVTENLAAPNVRDLDDISERGQLSFATLAE	62		
Qy	61	LLYRVRRFDLLKRILLKMDRAVETHLLRNPHLVSDYRVLVMSEIGE	105		
Dd	63	LLYRVRFDLLKRILTKDQATEVDHLNRNPHLVSDYRVLVMEICE	107		

RESULT 24
US-10-832-218-12
; Sequence 12, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
; APPLICANT: Tschoopp, Margot
; APPLICANT: Thome, Jurg
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmler, Marten

Query Match	74.9%	Score	390;	DB	17;	Length	481;
Best Local Similarity	75.3%	Pred. No.	1.7e-34;				
Matches	79;	Conservative	8;	Mismatches	18;	Indels	0;
Qy	1	KSMSAEVHQVBEALDTDEKEMLLFLCRDVAIDVPPNVRDLDLILRERKGLSVGDLAE	60				
Db	3	QSPVSAEVIHQVBEELDEDEKENMLFLCRDVTENLAAPNVRDLDLSLSEKGLSPATLAE	62				
Qy	61	LLYVRFRFDLLKRLKQWRKAVETHLLRNPHLVSDYRVLLMSEIGE	105				
Db	63	LLYVRFRFDLLKRLKTDKATVEDHLRRNPHLVSDYRVLLMEIGE	107				

```

; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-832-218-12

```

```

Query Match      74.9%; Score 390; DB 17; Length 481;
Best Local Similarity 75.2%; Pred. No. 1.7e-34;
Matches 79; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy  1 KRSMSAEVHQVTEALDTDEKEMLLFLCRDVAIDVPPNVRDLLDIIRBERGKLSVGDALAE 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  3 QSPVSAEVHQVBECLDEDEKENMLFLCRDVTENLAAPNVRDLLDSLSERGQLSFATLAE 62
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy  61 LLRYVRFDLLKRLIKMDRKAVENTHLLRNPHLYSDRYVLMSETGE 105
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  63 LLRYVRFDLLKRLIKTDKATVEDHLLRNPHLYSDRYVLLMEIGE 107
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 25
US-10-832-218-19
; Sequence 19, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
; APPLICANT: Techopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberley
; APPLICANT: Imrler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/10/8
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/410
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 1
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Ver9.1
; SEQ ID NO 19
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-832-218-19

```

Query Match	74.9%	Score	390;	DB	17;	Length	481;
Best Local Similarity	75.3%	Pred. No.	1.7e-34;				
Matches	79;	Conservative	8;	Mismatches	18;	Indels	0;
Qy	1	KSMSAEVHQVBEALDTDEKEMLLFLCRDVAIDVPPNVRDLDLILRERKGLSVGDLAE	60				
Db	3	QSPVSAEVIHQVBEELDEDEKENMLFLCRDVTENLAAPNVRDLDLSLSEKGLSPATLAE	62				
Qy	61	LLYVRFRFDLLKRLKQWRKAVETHLLRNPHLVSDYRVLLMSEIGE	105				
Db	63	LLYVRFRFDLLKRLKTDKATVEDHLRRNPHLVSDYRVLLMEIGE	107				

```
RESULT 26
US-10-005-921-2
; Sequence 2, Application US/10005921
; Publication No. US20020174450A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; APPLICANT: Leviten, Michael W.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CASH GENE
; TITLE OF INVENTION: DISRUPTIONS
; FILE REFERENCE: R-714
; CURRENT APPLICATION NUMBER: US/10/005,921
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/254,902
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-005-921-2

Query Match      74.9%; Score 390; DB 13; Length 484;
Best Local Similarity 75.2%; Pred. No. 1.7e-34;
Matches 79; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 KSRMSAEVHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDLRLRGKLSVGDIAE 60
   : : ||||| ||||| ||||| : : ||||| ||||| ||||| : : ||||| ||||| |||||
Db 3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLDSLSESGQLSPATLAE 62
   : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 LLYRVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIEGE 105
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 LLYRVRFDLLKRLKTKATVEDHLRRNPHLVSDYRVLMEIGE 107
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 27
US-10-849-901-5
; Sequence 5, Application US/10849901
; Publication No. US20040320039A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: GOLTSEV, Yura
; APPLICANT: KOVALENKO, Andrei
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BRODIANSKI, Vadim
; TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; FILE REFERENCE: WALLACH=23
; CURRENT APPLICATION NUMBER: US/10/849,901
; CURRENT FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/380,546
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/IL98/00098
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: IL 120367
; PRIOR FILING DATE: 1997-03-03
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-849-901-5

Query Match      74.9%; Score 390; DB 16; Length 484;
Best Local Similarity 75.2%; Pred. No. 1.7e-34;
Matches 79; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 KSRMSAEVHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLDLRLRGKLSVGDIAE 60
   : : ||||| ||||| ||||| : : ||||| ||||| ||||| : : ||||| ||||| |||||
Db 3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLDSLSESGQLSPATLAE 62
   : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 LLYRVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIEGE 105
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 LLYRVRFDLLKRLKTKATVEDHLRRNPHLVSDYRVLMEIGE 107
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 28
US-10-998-582-5
; Sequence 5, Application US/10998582
; Publication No. US20050152877A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: GOLTSEV, Yura
; APPLICANT: KOVALENKO, Andrei
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BRODIANSKI, Vadim
; TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; FILE REFERENCE: WALLACH=23
; CURRENT APPLICATION NUMBER: US/10/998,582
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US/09/380,546
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/IL98/00098
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: IL 120367
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: IL120759
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-998-582-5

Query Match      74.9%; Score 390; DB 18; Length 484;
Best Local Similarity 75.2%; Pred. No. 1.7e-34;
Matches 79; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 KSRMSAEVHQVEEALDTDEKEMMLFLCRDVAIDVVPNVRDLDLRLRGKLSVGDIAE 60
   : : ||||| ||||| ||||| : : ||||| ||||| ||||| : : ||||| ||||| |||||
Db 3 QSPVSAEVIHQVEECLDEDEKEMMLFLCRDVTENLAAPNVRDLDSLSESGQLSPATLAE 62
   : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 LLYRVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSIEGE 105
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 LLYRVRFDLLKRLKTKATVEDHLRRNPHLVSDYRVLMEIGE 107
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 29
US-09-410-194-2
; Sequence 2, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imbler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2005, 07:58:48 ; Search time 39 Seconds
(without alignments)
259.045 Million cell updates/sec

Title: US-09-402-569-2
Perfect score: 521
Sequence: 1 KSRMSAEVHQVEALDTDE.....LLRNPHLVSDYRVLMSEIGE 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121.5	23.3	241	2 T30761	hypothetical prote
2	119	22.8	371	2 T30762	hypothetical prote
3	99.5	19.1	171	2 S55668	hypothetical prote
4	83	15.9	208	2 A56912	FADD protein - hum
5	77.5	14.9	1207	2 A89822	RNA polymerase bet
6	77	14.8	312	2 D90198	transposase ISC123
7	77	14.8	319	2 D90350	transposase ISC123
8	77	14.8	319	2 E90466	transposase ISC123
9	77	14.8	917	2 T05430	hypothetical prote
10	75.5	14.5	1057	2 T10908	DNA-directed RNA p
11	75.5	14.5	1372	2 B71724	dna-directed RNA p
12	75.5	14.5	1399	2 G83112	DNA-directed RNA p
13	75	14.4	1401	2 G82336	DNA-directed RNA p
14	73.5	14.1	312	2 T37338	probable 35.9K pro
15	73.5	14.1	312	2 PN0121	l1L protein - vacc
16	73.5	14.1	312	2 E72157	l1L protein - vacc
17	73.5	14.1	312	2 F42510	l1L protein - vacc
18	73.5	14.1	312	2 T33070	l1L protein - vari
19	73.5	14.1	472	2 T27903	hypothetical prote
20	73.5	14.1	1372	2 F97722	hypothetical prote
21	73.5	14.1	1690	2 S41467	DNA-directed RNA p
22	73	14.0	319	2 D90344	transposase ISC123
23	73	14.0	319	2 D90342	transposase ISC123
24	73	14.0	319	2 S74012	hypothetical prote
25	73	14.0	319	2 H90321	transposase ISC123
26	73	14.0	319	2 G90428	transposase ISC123
27	73	14.0	1533	2 T00344	hypothetical prote
28	72.5	13.9	346	1 I48157	protein kinase (EC
29	72.5	13.9	348	2 B84448	hypothetical prote

30	72.5	13.9	485	1 JC4998	IMP dehydrogenase
31	72	13.8	151	2 H84033	transcription regu
32	71.5	13.7	486	1 E71456	IMP dehydrogenase
33	71.5	13.7	953	2 T46913	hypothetical prote
34	71.5	13.7	1377	2 C70148	DNA-directed RNA p
35	71.5	13.7	2890	2 B71846	dna-directed RNA p
36	71.5	13.7	2890	2 F64669	DNA-directed RNA p
37	71	13.6	785	2 D69985	DNA mismatch repai
38	71	13.6	1149	2 S67099	DNA-directed RNA p
39	70.5	13.5	168	2 T01482	hypothetical prote
40	70.5	13.5	932	2 F84465	hypothetical prote
41	70.5	13.5	953	2 S13520	coat protein beta
42	70.5	13.5	1048	2 T23764	hypothetical prote
43	70.5	13.5	1199	2 G69698	RNA polymerase (be
44	70.5	13.5	1316	2 G70535	probable rpoC prot
45	70	13.4	327	2 S08055	hypothetical prote

ALIGNMENTS

RESULT 1

T30761
hypothetical protein 159L - Molluscum contagiosum virus 1
N;Alternate names: MC159L
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T30761
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A;Reference number: Z20876; MUID:96325459; PMID:8670425
A;Accession: T30761
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-241 <SEN>
A;Cross-references: UNIPROT:Q98325; EMBL:U60315; PIDN:AAC55287.1
C;Genetics:
A;Note: MC159L

Query Match 23.3%; Score 121.5; DB 2; Length 241;
Best Local Similarity 36.5%; Pred. No. 0.00026;
Matches 35; Conservative 16; Mismatches 40; Indels 5; Gaps 3;

QY	10	HQVEALDTDEKEMLLFLCRDVAIDVVPNVRDLDLILRERKLSVGDLAELLYRVRFD	69
DB	15	HLLEE-LDSHEDSLFLCHDAAPGCT--TVTQALCSLSQQRKLTALALVEMLYVLQRM	71
QY	70	LLKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE	105
DB	72	LLKSRFGLSKEGAEQ--LLGTSFLTRYRKLIMVCVGE	105

RESULT 2

T30762
hypothetical protein 160L - Molluscum contagiosum virus 1
N;Alternate names: MC160L
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T30762
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A;Reference number: Z20876; MUID:96325459; PMID:8670425
A;Accession: T30762
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-371 <SEN>
A;Cross-references: UNIPROT:Q98326; EMBL:U60315; PIDN:AAC55288.1
C;Genetics:
A;Note: MC160L

Query Match 22.8%; Score 119; DB 2; Length 371;


```
Db      228 LDV-LPIIPPEIRPMAQL--DGGRFATSDLNDLYRRVINNRNRLKRLDLD 274
      || : : || : : : : : : : : || : : || : : || : : || : : || : :
RESULT 11
B71724
dna-directed RNA polymerase beta prime chain (rpoC) RP141 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: B71724
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: B71724
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1372 <AND>
A:Cross-references: UNIPROT:Q9ZE20; GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA1460
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: rpoC; RP141
C:Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match      14.5%; Score 75.5; DB 2; Length 1372;
Best Local Similarity 28.9%; Pred. No. 44;
Matches 26; Conservative 25; Mismatches 30; Indels 9; Gaps 6;

QY 1 KSRMSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVPVNRDLDIRRGKLSVGDIAE 60
      : : : : || : : || : : || : : || : : || : : || : : || : : ||
Db 213 KKKKLVKRLKLVDFLESENKPEWIM--DV-LPVIPPEIRPL--VMLDGGRFATSDLNE 267
      : : : : || : : || : : || : : || : : || : : || : : || : : ||
QY 61 LLVYR-RRFDLLKRLKMDRKAVETHLLRN 89
      || || || || : : : : || : : || : : || : : || : : || : : ||
Db 268 LYRRVINNRNRLKGLI--ESKAPDI-IVRN 294
      || || || || : : : : || : : || : : || : : || : : || : : ||

RESULT 12
G83112
DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain PA4269 [similarity] - Pseudomonas a
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83112
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1399 <STO>
A:Cross-references: UNIPROT:Q9HWC9; GB:AE004842; GB:AE004091; NID:g9950481; PIDN:AAG0765
A:Experimental source: strain PA01
C:Genetics:
A:Gene: rpoC; PA4269
C:Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain
C:Keywords: nucleotidyltransferase

Query Match      14.5%; Score 75.5; DB 2; Length 1399;
Best Local Similarity 23.0%; Pred. No. 45;
Matches 28; Conservative 25; Mismatches 30; Indels 39; Gaps 5;

QY 2 SRMSAEVIHQVEEALD-----TDEKEMLLFLCRDV----- 31
      : || : || : || : : : : : : : : : : : : : : : : : : : : : :
Db 178 ARGAEAHVHLLNAIDLEHIGRLREEIPQTNSETKIKLSKRLKLMLEAFQSGNKPWM 237
      : : : : || : : || : : || : : || : : || : : || : : || : : ||
QY 32 --AIDVPPVNRDLDIRRGKLSVGDIAELLYRV-RRFDLLKRLKMDRKAVETHLL 87
      : : || : : || : : || : : || : : || : : || : : || : : || : : ||
Db 238 VLTVPVLPDLPLVPL--DGGRFATSDLNDLYRRVINNRNRLKRLDLD---AAPDIIV 292
      : : || : : || : : || : : || : : || : : || : : || : : || : : ||
QY 88 RN 89
```

```
Db      293 RN 294
      ||
RESULT 13
G82336
DNA-directed RNA polymerase, beta' chain VC0329 [imported] - Vibrio cholerae (strain N16)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: G82336
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: G82336
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1401 <HEI>
A:Cross-references: UNIPROT:Q9KV29; GB:AE004121; GB:AE003852; NID:g9654739; PIDN:AAF93502
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0329
A:Map position: 1
C:Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match      14.4%; Score 75; DB 2; Length 1401;
Best Local Similarity 23.4%; Pred. No. 50;
Matches 33; Conservative 23; Mismatches 31; Indels 54; Gaps 7;

QY 2 SRMSAEVI-----HQVEEALDTDEKE-----M 23
      : : || : || : || : || : || : || : || : || : || : || : || : ||
Db 178 AKMGAEAIKDLLASMDLPAAEAQOMREELDTTNSETKRKKLTFRLLKLVFAVSGNKPWM 237
      : : || : || : || : || : || : || : || : || : || : || : || : ||
QY 24 LLFLCRDVAIDVVPVNRDLDIRRGKLSVGDIAELLYRV-RRFDLLKRLKMDRKAV 82
      : : || : || : || : : : : : : : : : : : : : : : : : : : : :
Db 238 IL-----TVLPVLPDLPLVPL--DGGRFATSDLNDLYRRVINNRNRLKRLLEL---AA 287
      : : || : || : || : || : || : || : || : || : || : || : || : ||

QY 83 ETHLLRNPHLYSDYRVLMSEI 103
      : : || : : || : : || : : || : : || : : || : : || : : || : : ||
Db 288 PDIIVRN-----EKKMLQESV 303
      : : || : : || : : || : : || : : || : : || : : || : : || : : ||

RESULT 14
T37338
Probable 35.9K protein - vaccinia virus (strain Ankara)
C:Species: vaccinia virus
A:Variety: strain Ankara
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 12-Jul-2004
C:Accession: T37338
R:Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
A:Reference number: Z20877
A:Accession: T37338
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-312 <ANT>
A:Cross-references: EMBL:U94848; PIDN:AAB96433.1
A:Experimental source: strain Ankara
C:Genetics:
A:Note: MVA062L
C:Superfamily: DNA-binding virion core protein, IL1 type

Query Match      14.1%; Score 73.5; DB 2; Length 312;
Best Local Similarity 25.6%; Pred. No. 13;
Matches 23; Conservative 26; Mismatches 30; Indels 11; Gaps 5;

QY 7 EVIHGV--EALDTPDEKEMLLFLCRDVAIDVVPVNRDLDIRRGKLSVGDIAELLYR 64
      : : || : : || : : || : : || : : || : : || : : || : : || : : ||
Db 158 DLINQLVKDESIOLEKSSI-----KD-SWYVIPD---ELIDVLKTRLFRSPQVKDNIISR 209
      : : || : : || : : || : : || : : || : : || : : || : : || : : ||
```

QY 65 VRFDLLKRILKMDRKAVETHLIRNPHLVS 94
 | : | | : | :: : || : |
Db 210 TRLDYDFTRVTKRDESIYY-ILKDPRIAS 238

RESULT 15

PNO121
IIL protein - vaccinia virus (strains L-IVP and WR)
C;Alternate names: 36k protein
C;Species: vaccinia virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 12-Jul-2004
C;Accession: PNO121; A29889
E;RJazankina, O.I.; Shchelkunov, S.N.; Muravlev, A.I.; Netesova, N.A.; Mikrjukov, N.N.; Mol. Biol. (Mosk.) 24, 968-976, 1990
A;Title: The molecular biological study of vaccinia virus genome II; localization and distribution of proteins in infected cells.
A;Reference number: PNO119; MUID:91066899; PMID:2250685
A;Accession: PNO121
A:Molecule type: DNA
A;Residues: 1-312 <RNA>
A;Experimental source: strain L-IVP
R;Schmitt, J.F.C.; Stunnenberg, H.G.
J. Virol. 62, 1889-1897, 1988
A;Title: Sequence and transcriptional analysis of the vaccinia virus HindIII I fragment.
A;Reference number: A29889; MUID:88215015; PMID:2835495
A;Accession: A29889
A:Molecule type: DNA
A;Residues: 1-20 <SH>
A;Cross-references: GB:J03399; NID:g335662; PIDN:AAB59803.1; PID:g555408
A;Experimental source: strain WR
C;Genetics:
A;Gene: IL1
C;Superfamily: DNA-binding virion core protein, IIL type
C;Keywords: glycoprotein; late protein
F;292,304/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.1%; Score 73.5; DB 2; Length 312;
Best Local Similarity 25.6%; Pred.No.13;
Matches 23; Conservative 26; Mismatches 30; Indels 11; Gaps 5;

QY 7 EVIHQV--EBALDTDEXEMILLFLCRDVAIDVPPNVNRDLLDLIRERKGLSVGDLAEIIYL 64
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 158 LLNLVKDSIQLEKSS-----KM-VMPDP---ELIDVLKTRLFRSPQVDKIISR 209

QY 65 VRFDLLKRILKMDRKAVETHLIRNPHLVS 94
 | : | | : | :: : || : |
Db 210 TRLDYDFTRVTKRDESIYY-ILKDPRIAS 238

RESULT 16

E72157
LiL protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 12-Jul-2004
C;Accession: E72157
R;Shchelkunov, S.N.; Totmenin, A.V.; Guttorov, V.V.; Safronov, P.P.; Maessung, R.F.; Lopatin, D.S.; et al., submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor virus.
A;Reference number: A72150
A;Accession: E72157
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-312 <SHC>
A;Cross-references: GB:I67780; NID:g5830555; PIDN:CAB54655.1; PID:g5830616
A;Experimental source: strain Garcia-1966
C;Genetics:
A;Gene: LiL
C;Superfamily: DNA-binding virion core protein, IIL type

Query Match 14.1%; Score 73.5; DB 2; Length 312;
Best Local Similarity 25.6%; Pred.No.13;
Matches 23; Conservative 26; Mismatches 30; Indels 11; Gaps 5;

QY 7 EVIHQV--EBALDTDEXEMILLFLCRDVAIDVPPNVNRDLLDLIRERKGLSVGDLAEIIYL 64


```
Query Match      14.0%; Score 73; DB 2; Length 319;
Best Local Similarity 34.2%; Pred. No. 14;
Matches 25; Conservative 16; Mismatches 28; Indels 4; Gaps 3;

QY 23 MLLFLC--RDVAIDVVPNPVRDLILRERKLSVGDLAELLYRVRFFDLKRLKMDRK 80
DB 66 MVLVSCSYRD-AVKMNVNVVAVFVGRKVGKSTLHDFVGRLYGVRRK-KLLEISFKLEEK 123

QY 81 AVETHLLRNPHLV 93
DB 124 CLPSYLPASAHLV 136

RESULT 23
D90342
transposase ISC1234 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: D90342
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90342
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KUR>
A;Cross-references: UNIPROT:Q97XEB; GB:AE006641; NID:gl3815051; PIDN:AAK41995.1; GSPDB:G
C;Genetics:
C;Superfamily: Sulfolobus solfataricus hypothetical protein c0626

Query Match      14.0%; Score 73; DB 2; Length 319;
Best Local Similarity 34.2%; Pred. No. 14;
Matches 25; Conservative 16; Mismatches 28; Indels 4; Gaps 3;

QY 23 MLLFLC--RDVAIDVVPNPVRDLILRERKLSVGDLAELLYRVRFFDLKRLKMDRK 80
DB 66 MVLVSCSYRD-AVKMNVNVVAVFVGRKVGKSTLHDFVGRLYGVRRK-KLLEISFKLEEK 123

QY 81 AVETHLLRNPHLV 93
DB 124 CLPSYLPASAHLV 136

RESULT 24
S74012
hypothetical protein c0626 - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S74012
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.
Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: 1
A;Reference number: S73076; MUID:97055432; PMID:8899719
A;Accession: S74012
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-319 <SEN>
A;Cross-references: UNIPROT:P95873; EMBL:Y08256; NID:gl1707679; PID:gl1707705
A;Experimental source: strain p2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Superfamily: Sulfolobus solfataricus hypothetical protein c0626

Query Match      14.0%; Score 73; DB 2; Length 319;
Best Local Similarity 34.2%; Pred. No. 14;
Matches 25; Conservative 16; Mismatches 28; Indels 4; Gaps 3;

QY 23 MLLFLC--RDVAIDVVPNPVRDLILRERKLSVGDLAELLYRVRFFDLKRLKMDRK 80
DB 66 MVLVSCSYRD-AVKMNVNVVAVFVGRKVGKSTLHDFVGRLYGVRRK-KLLEISFKLEEK 123
```

```
QY 81 AVETHLLRNPHLV 93
DB 124 CLPSYLPASAHLV 136
```

RESULT 25

```
H90321
transposase ISC1234 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90321; P90429; G90306; G90294; D90352
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90321
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KUR>
A;Cross-references: UNIPROT:Q97TU6; GB:AE006641; NID:gl3814857; PIDN:AAK41831.1; GSPDB:G
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KU2>
A;Cross-references: GB:AE006641; NID:gl3815869; PIDN:AAK42693.1; GSPDB:GN00155
A;Accession: C90306
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KU3>
A;Cross-references: GB:AE006641; NID:gl3814708; PIDN:AAK41706.1; GSPDB:GN00155
A;Accession: G90299
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KU4>
A;Cross-references: GB:AE006641; NID:gl3814644; PIDN:AAK41654.1; GSPDB:GN00155
A;Accession: D90294
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KU5>
A;Cross-references: GB:AE006641; NID:gl3814591; PIDN:AAK41611.1; GSPDB:GN00155
A;Accession: D90352
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KU6>
A;Cross-references: GB:AE006641; NID:gl3815143; PIDN:AAK42075.1; GSPDB:GN00155
C;Genetics:
C;Superfamily: Sulfolobus solfataricus hypothetical protein c0626
```

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Query Match      14.0%; Score 73; DB 2; Length 319;
Best Local Similarity 34.2%; Pred. No. 14;
Matches 25; Conservative 16; Mismatches 28; Indels 4; Gaps 3;
```

```
QY 23 MLLFLC--RDVAIDVVPNPVRDLILRERKLSVGDLAELLYRVRFFDLKRLKMDRK 80
DB 66 MVLVSCSYRD-AVKMNVNVVAVFVGRKVGKSTLHDFVGRLYGVRRK-KLLEISFKLEEK 123
```

```
QY 81 AVETHLLRNPHLV 93
DB 124 CLPSYLPASAHLV 136
```

RESULT 26

```
G90428
transposase ISC1234 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: G90428
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
```


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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2005, 07:58:49 ; Search time 58 Seconds
(without alignments)
927.040 Million cell updates/sec

Title: US-09-402-569-2
Perfect score: 521
Sequence: 1 KSRMAEVHQVEALDTDE.....LLRNPHLVSDYRVLMSGE 105

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	504	96.7	480	1 CFLA HUMAN	O15519 h casp8 and
2	437	83.9	219	2 Q6QN98	Q6qn98 sus scrofa
3	437	83.9	487	2 Q6QN97	Q6qn97 sus scrofa
4	399	76.6	218	2 Q9NMZ5	Q9nmz5 rattus norv
5	390	74.9	481	2 Q812G4	Q812g4 mus musculu
6	390	74.9	484	1 CFLA MOUSE	O35732 m casp8 and
7	154.5	29.7	497	2 Q6NTR7	Q6ntr7 xenopus lae
8	148	28.4	418	2 Q8UUG5	Q8uug5 brachydanio
9	129.5	24.9	188	2 P88961	P88961 human herp
10	121.5	23.3	241	1 CFLA MCV1	Q98325 molluscum c
11	120	23.0	476	2 Q661I9	Q661i9 brachydanio
12	120	23.0	476	2 Q918J3	Q918j3 brachydanio
13	119	22.8	369	2 O11300	O11300 molluscum c
14	119	22.8	371	2 Q98326	Q98326 molluscum c
15	115.5	22.2	482	2 Q90WU1	Q90wu1 gallus gall
16	114.5	22.0	480	1 ICEB MOUSE	O90110 mus musculu
17	106.5	20.4	482	2 Q9JHX4	Q9jhx4 rattus norv
18	104.5	20.1	182	2 Q99CX0	Q99cx0 bovine herp
19	104.5	20.1	500	2 Q91B64	Q91b64 xenopus lae
20	99.5	19.1	171	1 CFLA ERV2	Q66674 equine herp
21	98.5	18.9	278	2 Q6NV12	Q6nv12 homo sapien
22	98.5	18.9	479	1 ICEB HUMAN	O14790 h caspase-8
23	93	17.9	512	2 Q6PAD9	Q6pad9 xenopus lae
24	83	15.9	208	1 PADD HUMAN	Q13158 homo sapien
25	81	15.5	1388	2 Q6MDM0	Q6mdm0 parachlamyd
26	79	15.2	247	2 Q68HC0	Q68hc0 homo sapien
27	79	15.2	455	2 Q6KF63	Q6kfe3 homo sapien
28	79	15.2	478	2 Q6KF62	Q6kfe2 homo sapien
29	79	15.2	521	1 ICEA HUMAN	Q92851 homo sapien
30	79	15.2	522	2 Q81UF5	Q81uf5 homo sapien
31	79	15.2	730	2 Q86M65	Q86m65 trypanosoma

RESULT 1					
ID	CFLA HUMAN	STANDARD;	PRT;	480 AA.	
AC	O15519;	O14674;	O15137;	O15138;	O15356;
AC	O43618;	O43619;	O43620;	O60458;	O60459;
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	25-OCT-2004	(Rel. 45, Last annotation update)			
DE	CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like inhibitory protein) (C-FLIP) (Caspase-eight-related protein) (Casper)				
DE	(Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related inducer of toxicity) (MRIT) (Caspase homolog) (CASH) (Inhibitor of FLICE) (I-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1) (Usurpin).				
GN	Name=CFLAR; Synonyms=CASH, CLARP, MRIT;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 13 AND 14), AND MUTAGENESIS OF TYR-360.				
RC	TISSUE=Embryonic kidney, and Umbilical vein endothelial cells;				
RX	MEDLINE=97352452; PubMed=9208847; DOI=10.1016/S1074-7613(00)80450-1;				
RA	Shu H.-B., Halpin D.R., Goeddel D.V.;				
RL	"Casper is a FADD- and caspase-related inducer of apoptosis.";				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).				
RX	MEDLINE=97470967; PubMed=9326610; DOI=10.1073/pnas.94.21.11333;				
RA	Han D.K.M., Chaudhary P.M., Wright M.E., Friedman C., Traek B.J., Riedel R.T., Baskin D.G., Schwartz S.M., Hood L.;				
RT	"MRIT, a novel death-effector domain-containing protein, interacts with caspases and BclXL and initiates cell death.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 94:11333-11338(1997).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RC	TISSUE=Peripheral blood lymphocytes;				
RX	MEDLINE=97373543; PubMed=9217161; DOI=10.1038/40657;				
RA	Irmiler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V., Bodmer J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi D., French L.E., Tschoopp J.;				
RT	"Inhibition of death receptor signals by cellular FLIP.";				
RL	Nature 388:190-195(1997).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 8; 9 AND 10), AND MUTAGENESIS OF ASP-376.				
RC	TISSUE=T-cell;				
RX	MEDLINE=97373543; PubMed=9228018; DOI=10.1074/jbc.272.30.18542;				
RA	Srinivasula S.M., Ahmad M., O'Tillie S., Bullrich F., Banks S., Wang Y., Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J., Armstrong R.C., Alnemri E.S.;				
RT	"FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates Fas/TNFR1-induced apoptosis.";				

Q6q8z3 uncultured
Q6ap77 desulfotale
Q72hm6 thermus the
Q8q88 thermus the
P51586 plectonema
Q7zxx2 xenopus lae
Q8241 enterococcu
Q61c91 homo sapien
P94866 leuconostoc
P95688 staphylococ
Q65b4 bacillus li
P60284 staphylococ
P60285 staphylococ
P60286 staphylococ

RL J. Biol. Chem. 272:18542-18545(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Umbilical vein endothelial cells;
 RA MEDLINE=97362203; PubMed=9211860; DOI=10.1074/jbc.272.28.17255;
 RX Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.;
 RT "I-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and
 CD-95-induced apoptosis";
 RL J. Biol. Chem. 272:17255-17257(1997).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).
 RA Hu S., Dixit V.M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12).
 RC TISSUE=Kidney;
 RX MEDLINE=99218584; PubMed=10200473;
 RA Rasper D.M., Vaillancourt J.P., Hadano S., Houtzager V.M., Seiden I.,
 RA Keen S.L.C., Tawa P., Xanthoudakis S., Nasir J., Martindale D.,
 RA Koop B.P., Peterson E.P., Thornberry N.A., Huang J., Macpherson D.P.,
 RA Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S.,
 RA Nicholson D.W.;
 RT "Cell death attenuation by 'Usurpin', a mammalian DED-caspase
 homologue that precludes caspase-8 recruitment and activation by the
 CD-95 (Fas, APO-1) receptor complex.";
 RL Cell Death Differ. 5:271-288(1998).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Skin fibroblast;
 RX MEDLINE=97426025; PubMed=9289491; DOI=10.1074/jbc.272.32.19641;
 RA Golteev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
 RA Brodianskii V.M., Wallach D.;
 RT "CASH, a novel caspase homologue with death effector domains.";
 RL J. Biol. Chem. 272:19641-19644(1997).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Colon carcinoma;
 RX MEDLINE=98021435; PubMed=9380701; DOI=10.1073/pnas.94.20.10717;
 RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
 RT "CLARP, a death effector domain-containing protein interacts with
 caspase-8 and regulates apoptosis";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM 11).
 RX MEDLINE=21100893; PubMed=11161814; DOI=10.1006/geno.2000.6392;
 RA Hadano S., Yanagisawa Y., Skaug J., Ficher K., Nasir J.,
 RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
 RA Ikeda J.-E., Hayden M.R.;
 RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
 and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
 critical region at chromosome 2q33-q34: candidate genes for ALS2.";
 RL Genomics 71:200-213(2001).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph;
 RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP FUNCTION.
 RX MEDLINE=9908897; PubMed=9889531;
 RA Scalfidi C., Schmitz I., Krammer P.H., Peter M.E.;
 RT "The role of c-FLIP in modulation of CD95-induced apoptosis.";
 RL J. Biol. Chem. 274:1541-1548(1999).
 RN [13]
 RP INDUCTION.
 RX MEDLINE=99244884; PubMed=10227994;
 RA Algecras-Schmich A., Griffith T.S., Lynch D.H., Paya C.V.;
 RT "Cell cycle-dependent regulation of FLIP levels and susceptibility to
 Fas-mediated apoptosis";
 RL J. Immunol. 162:5205-5211(1999).
 RN [14]
 RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
 RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
 RA Hillman R.T., Green R.E., Brenner S.E.;
 RT "An unappreciated role for RNA surveillance";
 RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
 CC -!- FUNCTION: Apoptosis regulator protein which may function as a
 crucial link between cell survival and cell death pathways in
 mammalian cells. Acts as an inhibitor of TNFRSF6 mediated
 apoptosis. A proteolytic fragment (p43) is likely retained in the
 death-inducing signaling complex (DISC) thereby blocking further
 recruitment and processing of caspase-8 at the complex. Full
 length and shorter isoforms have been shown either to induce
 apoptosis or to reduce TNFRSF-triggered apoptosis. Lacks enzymatic
 (caspase) activity.
 CC -!- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-
 inducing signaling complex (DISC) formed by TNFRSF6, FADD and
 caspase-8. A proteolytic fragment (p43) stays associated with the
 DISC. Also interacts with caspase-10, caspase-3, TRAF1, TRAF2 and
 Bcl-X(L) (in vitro).
 CC -!- ALTERNATIVE PRODUCTS:
 Name=1; Synonyms=FLIP-L, CLARP1, MRIT alpha-1, CASH alpha, I-FLICE
 1, FLAME-1 gamma, Usurpin alpha;
 IsoId=O15519-1; Sequence=Displayed;
 Name=2; Synonyms=FLIP-S, CLARP2, MRIT beta-1, CASH beta;
 IsoId=O15519-2; Sequence=VSP_000828, VSP_000829;
 Name=3; Synonyms=MRIT alpha-2;
 IsoId=O15519-3; Sequence=VSP_000824, VSP_000838;
 Name=4; Synonyms=I-FLICE 2;
 IsoId=O15519-4; Sequence=VSP_000825;
 Name=5; Synonyms=I-FLICE 3;
 IsoId=O15519-5; Sequence=VSP_000840;
 Name=6; Synonyms=I-FLICE 4;
 IsoId=O15519-6; Sequence=VSP_000826, VSP_000841;
 Name=7; Synonyms=I-FLICE 5;
 IsoId=O15519-7; Sequence=VSP_000824, VSP_000827, VSP_000838;
 Name=8; Synonyms=Flame-1 alpha;
 IsoId=O15519-8; Sequence=VSP_000830;
 Name=9; Synonyms=Flame-1 beta;
 IsoId=O15519-9; Sequence=VSP_000830, VSP_000836, VSP_000837;
 Note=May be produced at very low levels due to a premature stop
 codon in the mRNA, leading to nonsense-mediated mRNA decay;
 Name=10; Synonyms=Flame-1 delta;
 IsoId=O15519-10; Sequence=VSP_000834, VSP_000835;
 Name=11; Synonyms=Usurpin beta;
 IsoId=O15519-11; Sequence=VSP_000838;
 Name=12; Synonyms=Usurpin gamma;
 IsoId=O15519-12; Sequence=VSP_000832, VSP_000833;
 Name=13;
 IsoId=O15519-13; Sequence=VSP_000831;
 Name=14;
 IsoId=O15519-14; Sequence=VSP_000839;
 CC -!- TISSUE SPECIFICITY: Widely expressed. Higher expression in
 skeletal muscle, pancreas, heart, kidney, placenta, and peripheral
 blood leukocytes. Also detected in diverse cell lines. Isoform 8
 is predominantly expressed in testis and skeletal muscle.

CC -I- INDUCTION: Repressed by IL-2 after TCR stimulation, during progression to the S-phase of the cell cycle.

Query Match 96.7%; Score 504; DB 1; Length 480;
 Best Local Similarity 99.0%; Pred. No. 5.8e-39;
 Matches 101; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MSAEVHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGLAEALL 63
 DB 1 MSAEVHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGLAEALL 60
 QY 64 RVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
 DB 61 RVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 102

RESULT 2
 Q6QN98 PRELIMINARY; PRT; 219 AA.
 AC Q6QN98;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Cellular FLICE-like inhibitory protein short form.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Goto Y., Maeda A., Matsuda F., Inoue N., Manabe N.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY533020; AAS22337.1; -;
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR01875; DED.
 DR Pfam; PF01335; DED; 2.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; P550168; DED; 2.
 SQ SEQUENCE 219 AA; 25303 MW; 840DC7135D88AAC8 CRC64;

Query Match 83.9%; Score 437; DB 2; Length 219;
 Best Local Similarity 85.4%; Pred. No. 4.7e-33;
 Matches 88; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 QY 3 RMSAEVHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGLAEALL 62
 DB 5 RMSAEVHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGLAEALL 64
 QY 63 YVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
 DB 65 YVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 107

RESULT 3
 Q6QN97 PRELIMINARY; PRT; 487 AA.
 AC Q6QN97;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Cellular FLICE-like inhibitory protein long form.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Goto Y., Maeda A., Matsuda F., Inoue N., Manabe N.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY533021; AAS22337.1; -;
 DR HSSP; P55211; 1JXQ.

DR GO; GO:0030693; F:caspace activity; IEA.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF01335; DED; 2.
 DR SMART; SM00115; CASc; 1.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; P550208; CASPASE_P20; 1.
 DR PROSITE; P550168; DED; 2.
 SQ SEQUENCE 487 AA; 56000 MW; 067BE3618EE9C0E7 CRC64;

Query Match 83.9%; Score 437; DB 2; Length 487;
 Best Local Similarity 85.4%; Pred. No. 1.1e-32;
 Matches 88; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 QY 3 RMSAEVHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGLAEALL 62
 DB 5 RMSAEVHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGLAEALL 64
 QY 63 YVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
 DB 65 YVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 107

RESULT 4
 Q99MZ5 PRELIMINARY; PRT; 218 AA.
 AC Q99MZ5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE FLIP short form.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=22131045; PubMed=12135878;
 RA Xiao C.W., Assefin E., Tsang B.K.;
 RT "Nuclear factor kappaB-mediated induction of Flce-like inhibitory protein prevents tumor necrosis factor alpha-induced apoptosis in rat granulosa cells";
 RL Biol. Reprod. 67:436-441(2002).
 DR EMBL; AF244366; AAK28358.1; -;
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR001875; DED.
 DR Pfam; PF01335; DED; 2.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; P550168; DED; 2.
 SQ SEQUENCE 218 AA; 24718 MW; 9DA9EBAF3441967B CRC64;

Query Match 76.6%; Score 399; DB 2; Length 218;
 Best Local Similarity 76.9%; Pred. No. 1.7e-29;
 Matches 80; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 2 RMSAEVHQVEEALDTDEKEMLLFLCRDVAIDVVPNVRDLILRERKLSVGLAEALL 61
 DB 4 STVSAEVIHQVEEALDTDEKEMLLFLCRDVTENLAPPNVRDLILRERKLSVGLAEALL 63
 QY 62 LYVRRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
 DB 64 LYVRRFDLLKRLKMDRKAAVEDHLCRSPHLVSDYRVLMSEIGE 107

RESULT 5

RESULT 6

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[1]
SEQUENCE FROM N.A.
RN RP
RC TISSUE=Ovary;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodryguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerrch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RN RP
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RN Dev. Dyn. 225:384-391(2002).
[3]
SEQUENCE FROM N.A.
RN RP
RC TISSUE=Ovary;
RA Klein S., Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC068888; AAHG68888.1; -.
DR HSSP; P5211; 1JXQ.
DR GO; GO:0030693; F:caspace activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR PRINTS; PR00376; IL1BENZYM.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS50208; CASPASE_p20; 1.
DR PROSITE; PS50168; DED; 2.
DR Hypothetical protein.
FT NON TER
FT 1
SEQUENCE 497 AA; 56872 MW; 1872F291010F83BF CRC64;

Query Match 29.7%; Score 154.5; DB 2; Length 497;
Best Local Similarity 38.8%; Pred.No. 3.6e-06;
Matches 38; Conservative 15; Mismatches 42; Indels 3; Gaps 1

QY 8 VTHQVEALDTDEKEMLLFLCRDVAIDVPNPVRDLLDLIRBERGKLSVGDGLAELLYRVR 67
Db 50 ILQLSDELDAAEAGLFLCRD---NSSKTNVRDLLEDINDYSSIPFGLAEVLVYKR 106
QY 68 FDLKRLKMDRKAVETHLLRNPHLYSDYRVLMSGE 105
Db 107 FDLKXKLYLTKATVENLLKSRSSIPFSYSLMVGISE 144

RESULT 8
Q8UUVG5

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Db 5 EVCEVARKGTDREVVFLP---LNVFIPQPTLAQIGALRAKLBEGRLTFFLLAECLF 61
QY 64 RVRFDLKRLKMDRKAVETHLLRNPHLVSDYRVLMSEI-GE 105
Db 62 RAGRDLLRDLHDPFLERHLAGTMSYSPQTLVLHVDGE 104

RESULT 10
CFLA_MCV1
ID _CFLA_MCV1 STANDARD; PRT; 241 AA.
AC Q98325; O11298;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Viral CASP8 and FADD-like apoptosis regulator (v-CFLAR) (Viral FLICE-
inhibitory protein) (v-FLIP).
GN Name=159L; Synonyms=H-H2.2;
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96325459; PubMed=8670425;
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
Moss B.;
RT "Genome sequence of a human tumorigenic poxvirus: prediction of
specific host response-evasion genes.";
RL Science 273:813-816(1996).
RN [2]
RP SEQUENCE OF 91-241 FROM N.A.
RX MEDLINE=97352177; PubMed=9208457; DOI=10.1023/A:1007991508159;
RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.;
RT "A random DNA sequencing, computer-based approach for the generation
of a gene map of Molluscum contagiosum virus.";
RL Virus Genes 14:73-80(1997).
RN [3]
RP FUNCTION.
RX MEDLINE=97242415; PubMed=9087414;
RA Thome M., Schneider P., Hofmann K., Fickenscher H., Meinel E.,
Neipel F., Mattmann C., Burns K., Bodmer J.-L., Schroeter M.,
Scalfidi C., Krammer P.H., Peter M.E., Tschopp J.;
RT "Viral FLICE-inhibitory proteins (Flips) prevent apoptosis induced by
death receptors.";
RL Nature 386:517-521(1997).
RN [4]
RP FUNCTION.
RX MEDLINE=97188440; PubMed=9037025; DOI=10.1073/pnas.94.4.1172;
RA Bertin J., Armstrong R.C., Otfillie S., Martin D.A., Wang Y., Banks S.,
Wang G.-H., Senkevich T.G., Alnemri E.S., Moss B., Lenardo M.J.,
Tomaseelli K.J., Cohen J.I.;
RT "Death effector domain-containing herpesvirus and poxvirus proteins
inhibit both Fas- and TNFR1-induced apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:1172-1176(1997).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=99457304; PubMed=10526240;
RA Taakmo S.I., Yonehara S.;
RT "Requirement of cooperative functions of two repeated death effector
domains in caspase-8 and in MC159 for induction and inhibition of
apoptosis, respectively.";
RL Genes Cells 4:541-549(1999).
CC -!- FUNCTION: Inhibits TNFRSF1A, TNFRSF6 and TNFRSF12 induced
apoptosis. May interfere with caspase-8 recruitment and activation
at the death-inducing signaling complex (DISC). May lead to higher
virus production and contribute to virus persistence and
oncogenicity.
CC -!- SUBUNIT: Associates with the death-inducing signaling complex
(DISC) formed by TNFRSF6, FADD and caspase-8. Interacts with FADD.
CC -!- SIMILARITY: Contains 2 death effector (DED) domains.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U60315; AAC55287.1; -
DR EMBL; U66888; AAB57923.1; -
DR PIR; T30761; T30761.
DR InterPro: IPR011029; DEATH_like.
DR InterPro: IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0168; DED; 2.
KW Apoptosis; Repeat.
FT DOMAIN 8 78 DED 1.
FT DOMAIN 95 175 DED 2.
SQ SEQUENCE 241 AA; 26939 MW; 155C9FB0B969E216 CRC64;

Query Match 23.3%; Score 121.5; DB 1; Length 241;
Best Local Similarity 36.5%; Pred. No. 0.002;
Matches 35; Conservative 16; Mismatches 40; Indels 5; Gaps 3;

QY 10 HOVERALDTDEKEMLLFLCRDVAIDVPPNVRDLDIRERKLSVGDIAELLYRVRRPD 69
Db 15 HLLEE-LDSHEDSLFLCHDAAPGCT--TVTQALCSLSQQRKLTALALVEMLYVLQRM 71
QY 70 LUKRILKMDRKAVETHLLRNPHLVSDYRVLMSEIGE 105
Db 72 LLKSRFGSLSGAEQ--LLGTSFLTRYRKLMLVCVGE 105

RESULT 11
Q66119 PRELIMINARY; PRT; 476 AA.
AC Q66119;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Caspase 8.
GN Name=casp8;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]_TaxID=7955;
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

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RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Director MC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081583; AAH81583.1; -.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 476 AA; 54963 MW; 2EA22110F14C1E01 CRC64;

Query Match      23.0%; Score 120; DB 2; Length 476;
Best Local Similarity 33.6%; Pred. No. 0.006;
Matches 38; Conservative 23; Mismatches 36; Indels 16; Gaps 5;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVP-----PNVRDLDDLRLRERKLSVG 56
Db 1 MDPQIFHEIDENLTSGVDQLKFLC----LDPIPKRRLSVTDKDLILRLDEQGLLEDE 56
QY 57 DL-AELLYVRRFDLLKRLKMDRKAVETHLLRNPHL----VSDYRVLMSEIGE 105
Db 57 LLFPELLITIGRIDLLE-ILKKSKEVERNLLRCDNSRKGVSAVRKMLLKISE 108

RESULT 12
Q918J3 PRELIMINARY; PRT; 476 AA.
AC Q918J3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-8.
GN Name=casp8;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
CC -1- SIMILARITY: Belongs to the peptidase C14 family.
DR EMBL; AF273220; AAF79207.1; -.
DR HSP; OSC0K4; 1QTN.
DR ZFIN; ZDB-GENE-000713-1; casp8.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 2.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00031; CASC; 1.
DR SMART; SM00115; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.

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DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 476 AA; 54889 MW; FD9DF4B3C3C1FB9 CRC64;

Query Match      23.0%; Score 120; DB 2; Length 476;
Best Local Similarity 33.6%; Pred. No. 0.006;
Matches 38; Conservative 23; Mismatches 36; Indels 16; Gaps 5;

QY 4 MSAEVIHQVEEALDTDEKEMLLFLCRDVAIDVVP-----PNVRDLDDLRLRERKLSVG 56
Db 1 MDPQIFHEIDENLTSGVDQLKFLC----LDPIPKRRLSVTDKDLILRLDEQGLLEDE 56
QY 57 DL-AELLYVRRFDLLKRLKMDRKAVETHLLRNPHL----VSDYRVLMSEIGE 105
Db 57 LLFPELLITIGRIDLLE-ILKKSKEVERNLLRCDNSRKGVSAVRKMLLKISE 108

RESULT 13
O11300 PRELIMINARY; PRT; 369 AA.
AC O11300;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein H-K.1 (Fragment).
GN Name=H-K.1;
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97352177; PubMed=9208457; DOI=10.1023/A:1007991508159;
RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
RA Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.;
RT "A random DNA sequencing, computer-based approach for the generation of a gene map of molluscum contagiosum virus.";
RL Virus Genes 14:73-80(1997).
DR EMBL; U86889; AAB57924.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0168; DED; 2.
KW Hypothetical protein.
FT NON_TER 369
SQ SEQUENCE 369 AA; 38403 MW; FECD119A576FF001 CRC64;

Query Match      22.8%; Score 119; DB 2; Length 369;
Best Local Similarity 38.6%; Pred. No. 0.0056;
Matches 34; Conservative 12; Mismatches 38; Indels 4; Gaps 2;

QY 16 LDTDEKEMLLFLCRDVAIDVVPNNVRDLDDLRLRERKLSVGDLAELLYVRRFDLLKRL 75
Db 18 LDASEHEVLRLCRDVA--PASKTAEDALRALQRRRLTLSSMAELLCALRFRDVLKVR 75
QY 76 KMDRKAVETHLLRNPHLYSDYRVLMSEI 103
Db 76 GMTRECAGR--LLGHGFLSYRVLQVAII 101

RESULT 14
Q98326 PRELIMINARY; PRT; 371 AA.
AC Q98326;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MC160L.
GN Name=MC160L;
OS Molluscum contagiosum virus subtype 1 (MCV1).

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it to either receptor. The resulting aggregate called death-inducing signaling complex (DISC) performs CASP8 proteolytic activation. The active dimeric enzyme is then liberated from the DISC and free to activate downstream apoptotic proteases. Proteolytic fragments of the N-terminal propeptide (termed CAP3, CAP5 and CAP6) are likely retained in the DISC. Cleaves and activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May participate in the G2M apoptotic pathways. Cleaves ADPRT. Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC. Likely target for the coxsack virus CRMA death inhibitory protein. ENZYME REGULATION: Inhibited by 2-VAD-FK, Crma and P35. SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit. Interacts with FADD, CFLAR and PEAL5 (By similarity). TISSUE SPECIFICITY: Expressed in a wide variety of tissues. Highest expression in spleen, thymus, lung, liver and kidney. Lower expression in heart, brain, testis and skeletal muscle. DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at day 7. PTM: Generation of the subunits requires association with the death-inducing signaling complex (DISC), whereas additional processing is likely due to the autocatalytic activity of the activated protease. GZMB and CASP10 can be involved in these processing events (By similarity). SIMILARITY: Belongs to the peptidase C14 family. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; AF067841; AAC40132.1; -. JOINED.
 EMBL; AF067835; AAC40132.1; JOINED.
 EMBL; AF067836; AAC40132.1; JOINED.
 EMBL; AF067837; AAC40132.1; JOINED.
 EMBL; AF067838; AAC40132.1; JOINED.
 EMBL; AF067839; AAC40132.1; JOINED.
 EMBL; AF067840; AAC40132.1; JOINED.
 EMBL; AF067834; AAC40131.1; -.
 EMBL; AJ007749; CAA06777.1; -.
 EMBL; BC006737; AAH06737.1; -.
 EMBL; BC049955; AAH49955.1; -.
 EMBL; AJ000641; CAA04196.1; -.
 HSSP; Q9C0K4; IQTN.
 MEROPS; C14.009; -.
 MGD; MGI:1261423; Casp8.
 GO; GO:0005737; C:cytoplasm; IDA.
 GO; GO:0005634; C:nucleus; IDA.
 GO; GO:0030693; F:caspace activity; IDA.
 GO; GO:0006915; P:apoptosis; IDA.
 InterPro; IPR011029; DEATH_like.
 InterPro; IPR001875; DEATH.
 InterPro; IPR002138; ICE p10.
 InterPro; IPR001309; ICE p20.
 InterPro; IPR002398; Peptidase_C14.
 Pfam; PF01335; DEB; 2.
 Pfam; PF00656; Peptidase_C14; 1.
 PRINTS; PR00376; ILIBENZYM.
 PROSITE; PS01122; CASPASE_CYS; 1.
 PROSITE; PS01121; CASPASE_HIS; 1.
 PROSITE; PS50207; CASPASE_P10; 1.
 PROSITE; PS50208; CASPASE_P10; 1.
 PROSITE; PS50208; CASPASE_P20; 1.
 PROSITE; PS50168; DEB; 2.
 Apoptosis; Hydrolyase; Repeat; Thiol protease; Zymogen.
 Apoptosis; Hydrolyase; Repeat; Thiol protease; Zymogen.
 PROPEP 1 218 By similarity.
 FT CHAIN 219 376 Caspase-8 subunit p18.
 FT CHAIN 377 387 By similarity.
 FT CHAIN 388 480 Caspase-8 subunit p10.
 FT ACT_SITE 319 319 By similarity.
 FT ACT_SITE 362 362 By similarity.

FT DOMAIN 3 80 DED 1.
 FT DOMAIN 101 177 DED 2.
 FT CONFLICT 68 71 HISR -> PHPVG (in Ref. 4).
 FT CONFLICT 94 99 DNAQIS -> RQCPRFL (in Ref. 4).
 FT CONFLICT 96 96 A -> V (in Ref. 2).
 FT CONFLICT 103 107 VMLFK -> SCSFR (in Ref. 4).
 FT CONFLICT 475 475 K -> N (in Ref. 4).
 SQ SEQUENCE 480 AA; 55356 MW; 045268AE3DE5ED4F CRC64;
 Query Match 22.0%; Score 114.5; DB 1; Length 480;
 Best Local Similarity 29.4%; Pred.No. 0.02; Indels 17; Gaps 5;
 Matches 32; Conservative 27; Mismatches 33;
 QY 9 IQVSEALDTDEKEMLLFLCRDVAIDVVPPNVRDLDD-----ILRRGKLSVGDLA-- 59
 Db 7 LYAIAEEIGSEDLAALKFLC-----LDYIPHKQETIEDAQKLFLLREKGMLEEGNLSFL 62
 QY 60 ELLVVRFRFDLLKRLKMDRKAVETHLLRNPH--LVSDYRVLMSIEIG 105
 Db 63 KELLPHISRWDLNVNFDLCNREEM-VRELDPDQAQISPYRVMLFKLSE 110
 RESULT 17
 Q9UHX4 PRELIMINARY; PRT; 482 AA.
 AC Q9JHX4;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Caspase-8.
 GN Name=CASP8;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley;
 RA Itoh T., Itoh A., Pleasure D.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Cerebellum;
 RA Cao G., Graham S.H., Chen D., Chen J.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the peptidase C14 family.
 DR EMBL; AF279308; AAF87778.1; -.
 DR EMBL; AF288372; AAK83055.1; -.
 DR HSSP; Q9C0K4; IQDU.
 DR MEROPS; C14.009; -.
 DR GO; GO:0030693; F:caspace activity; IEA.
 DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
 DR GO; GO:0036787; F:hydrolase activity; IEA.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR001875; DEB.
 DR InterPro; IPR002138; ICE p10.
 DR InterPro; IPR001309; ICE p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF01335; DEB; 2.
 DR PRINTS; PR00376; ILIBENZYM.
 DR SMART; SM00031; DEB; 2.
 DR SMART; SM00115; CASP; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hydrolase; Protease; Thiol protease; Zymogen.
 SQ SEQUENCE 482 AA; 55339 MW; 82B4A29330C53264 CRC64;

Query Match 20.4%; Score 106.5; DB 2; Length 482;
Best Local Similarity 30.8%; Pred. No. 0.11;
Matches 32; Conservative 21; Mismatches 44; Indels 7; Gaps 3;
QY 9 IHOVEALDTEKEMLLFLCRDVAIDVVPNVRLDLDI---LRERKGLSVGDLA---ELL 62
DB 7 LYDIAERLGNELAAKFLCLDHPKQKQBSINDVLVLFORLOEGWLEEDNLSFLKELL 66
QY 63 YRVRFEDLLKRLKMDRKAVETHL-IRNPHLVSDYRVLMSEIGE 105
DB 67 FHISRRDLKSLVKSPEEMVRELQVLGKAQVAYRVMLFKLSE 110
RESULT 18
Q99CX0 PRELIMINARY; PRT; 182 AA.
AC Q99CX0
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE V-FLIP.
OS Bovine herpesvirus 4 (BoHV-4) (Movar virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10385;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20583805; PubMed=11152491;
RX DOI=10.1128/JVI.75.3.1186-1194.2001;
RA Zimmermann W., Broll H., Ehlers B., Buhk H.-J., Rosenthal A.,
RA Goltz M.;
RT "Genome sequence of bovine herpesvirus 4, a bovine Rhadinovirus, and
RT identification of an origin of DNA replication.";
RL J. Virol. 75:1186-1194(2001).
DR EMBL; AF318573; AAK07993.1; -.
DR HSSP; Q9Z297; IN3K.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS00168; DED; 2.
SQ SEQUENCE 182 AA; 21792 MW; 73BF1ADD9B0FE6A6 CRC64;
Query Match 20.1%; Score 104.5; DB 2; Length 182;
Best Local Similarity 26.4%; Pred. No. 0.059;
Matches 28; Conservative 28; Mismatches 43; Indels 7; Gaps 3;
QY 4 MSAEVIHQVEALDTEKEMLLFLCRDVAIDVVPNVRLD---LDILRERKGLSVGDLA 60
DB 2 VTRDVLATETHLNQNEKTFVMYFLLD---PYIPKECEDFLPTLENLHSKRKIIYPILIE 58
QY 61 LLYRVRFEDLLKRLKMDRKAVETHLIRNP-HLVSDYRVLMSEIGE 105
DB 59 LMVILQRFDLRSIFLLDHRFVKDQITSSHWNVISPYKQLIFSIGQ 104
RESULT 19
Q9IB64 PRELIMINARY; PRT; 500 AA.
AC Q9IB64
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Caspase-8.
GN Name=Caspase-8;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739; DOI=10.1074/jbc.275.14.10484;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
RL J. Biol. Chem. 275:10484-10491(2000).
CC J- SIMILARITY: Belongs to the peptidase C14 family.
DR EMBL; AB038171; BAA94749.1; -.
DR HSSP; Q9C0K4; IQTN.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR000226; Interleukin_7_9.
DR Pfam; PF01335; DED; 2.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50168; DED; 2.
DR PROSITE; PS00255; INTERLEUKIN_7_9; UNKNOWN_1.
KW Hydrolase; Protease; Thiol protease; Zymogen.
SQ SEQUENCE 500 AA; 57623 MW; AE138D4145108AE2 CRC64;
Query Match 20.1%; Score 104.5; DB 2; Length 500;
Best Local Similarity 27.6%; Pred. No. 0.18;
Matches 29; Conservative 27; Mismatches 42; Indels 7; Gaps 3;
QY 7 EVIHQVEALDTEKEMLLFLCRDVAIDVVPNVRLD---LDILRERKGLSVGDLA---E 60
DB 19 KLLFEISDLDKNTETLAMIFLCEKRVTAQEKENINDAKTLFLCKKKDLICYNLSFLKE 78
QY 61 LLYRVRFEDLLKRLKMDRKAVETHLIRNPHLVSDYRVLMSEIGE 105
DB 79 LLYRIGRNDLLRGLKRVTEIKRIEVSPO-ISPYRILLYDISQ 122
RESULT 20
CFLA_EHV2 STANDARD; PRT; 171 AA.
ID CFLA_EHV2
AC Q66674;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Viral CASP8 and FADD-like apoptosis regulator (v-CFLAR) (Viral FLICE-
DE inhibitory protein) (v-FLIP).
GN Name=E8;
OS Equine herpesvirus 2 (strain 86/87) (EHV-2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=82831;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95302501; PubMed=7783207;
RA Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
RT "The DNA sequence of equine herpesvirus 2.";
RL J. Mol. Biol. 249:520-528(1995).
RN [2]
FUNCTION.
RP MEDLINE=97242415; PubMed=9087414;
RX Thome M., Schneider P., Hofmann K., Fickenscher H., Meinl E.,
RA Neipel F., Mattmann C., Burns K., Bodmer J.-L., Schroeter M.,
RA Scaffidi C., Kramer P.H., Peter M.E., Tschoopp J.;

- RA Boldin M.P., Goncharov T.M., Goltsev Y.V., Wallach D.;
 RT "Involvement of MACH, a novel MORIT/FADD-interacting protease, in
 RT Fas/APO-1- and TNF receptor-induced cell death."; [1]
 RL Cell 85:803-815(1996).
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE
 RX MEDLINE=96279827; PubMed=8681377; DOI=10.1016/S0092-8674(00)81266-0;
 RA Muzio M., Chinaiyana A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
 RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
 RA Krammer P.H., Peter M.E., Dixit V.M.;
 RT "FLICE, a novel FADD-homologous ICH/CED-3-like protease, is recruited
 RT to the CD95 (Fas/APO-1) death-inducing signaling complex."; [1]
 RL Cell 85:817-827(1996).
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=T-cell;
 RX MEDLINE=96353838; PubMed=8755496; DOI=10.1073/pnas.93.15.7464;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J.F., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains."; [1]
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99132295; PubMed=9931493; DOI=10.1016/S0378-1119(98)00565-4;
 RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
 RT "Structure and chromosome localization of the human CASP8 gene."; [1]
 RL Gene 226:225-232(1999).
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=97373543; PubMed=9228018; DOI=10.1074/jbc.272.30.18542;
 RA Srinivasula S.M., Ahmad M., Oltillie S., Bullrich F., Banks S.,
 RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
 RA Armstrong R.C., Alnemri E.S.;
 RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
 RT Fas/TNFR1-induced apoptosis."; [1]
 RL J. Biol. Chem. 272:18542-18545(1997).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21100893; PubMed=11161814; DOI=10.1006/geno.2000.6392;
 RA Hadano S., Yanagisawa Y., Staug J., Fichter K., Nasir J.,
 RA Randalde D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
 RA Ikeda J.-E., Hayden M.R.;
 RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
 RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
 RT critical region at chromosome 2q33-q34: candidate genes for ALS2."; [1]
 RL Genomics 71:200-213(2001).
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
 RC TISSUE=Leukocyte;
 RX MEDLINE=22005982; PubMed=12010809; DOI=10.1182/blood.V99.11.4070;
 RA Himeji D., Horiuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
 RA Harada M.;
 RT "Characterization of caspase-8L: a novel isoform of caspase-8 that
 RT behaves as an inhibitor of the caspase cascade."; [1]
 RL Blood 99:4070-4078(2002).
 RN
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 9), AND INTERACTION OF ISOFORM 9
 RP WITH BCL2 AT THE ENDOPLASMIC RETICULUM.
 RX MEDLINE=21927603; PubMed=11917123; DOI=10.1073/pnas.072088099;
 RA Breckenridge D.G., Nguyen M., Kupzig S., Reth M., Shore G.C.;
 RT "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
 RT complex at the endoplasmic reticulum."; [1]
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 7).
 RC TISSUE=Leukocyte;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshikiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguillano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield A.S.N., Krzyzinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra W.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."; [1]
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN
 RP PARTIAL SEQUENCE, AND PROCESSING.
 RX MEDLINE=97121412; PubMed=8962078; DOI=10.1073/pnas.93.25.14486;
 RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
 RA Alnemri E.S.;
 RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
 RT protease Mch5 is a CrmA-inhibitable protease that activates multiple
 RT Ced-3/ICE-like cysteine proteases."; [1]
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
 RN
 RP FUNCTION.
 RX MEDLINE=97160607; PubMed=9006941; DOI=10.1074/jbc.272.5.2952;
 RA Muzio M., Salvesen G.S., Dixit V.M.;
 RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
 RT zymogens."; [1]
 RL J. Biol. Chem. 272:2952-2956(1997).
 RN
 RP PROCESSING.
 RX MEDLINE=97327557; PubMed=9184224; DOI=10.1093/emboj/16.10.2794;
 RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
 RA Krammer P.H., Peter M.E.;
 RT "FLICE is activated by association with the CD95 death-inducing
 RT signaling complex (DISC)."; [1]
 RL EMBO J. 16:2794-2804(1997).
 RN
 RP CHARACTERIZATION OF ISOFORM 7.
 RX MEDLINE=20318377; PubMed=10860845; DOI=10.1006/bbrc.2000.2841;
 RA Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
 RA Hayashi K.;
 RT "Dominant expression of a novel splice variant of caspase-8 in human
 RT peripheral blood lymphocytes."; [1]
 RL Biochem. Biophys. Res. Commun. 272:877-881(2000).
 RN
 RP INTERACTIONS WITH BCL2; BCL2L1 AND BCL2L1.
 RX MEDLINE=97477382; PubMed=9334338; DOI=10.1083/jcb.139.2.327;
 RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
 RA Cronleigh J.A., Shore G.C.;
 RT "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
 RT endoplasmic reticulum."; [1]
 RL J. Cell Biol. 139:327-338(1997).
 RN
 RP INTERACTION WITH PEAL5.
 RX MEDLINE=99369240; PubMed=10442631; DOI=10.1038/aj.1202831;
 RA Condorelli G., Vigliotta G., Cafieri A., Trecia A., Andalo P.,
 RA Oriente F., Mele C., Caruso M., Formisano P., Beguinot F.;
 RT "PEP/PEA-15: an anti-apoptotic molecule that regulates Fas/TNFR1-
 RT induced apoptosis."; [1]
 RL Oncogene 18:4409-4415(1999).
 RN
 RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
 RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
 RA Hillman R.T., Green R.E., Brenner S.E.;
 RT "An unappreciated role for RNA surveillance."; [1]
 RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=99451259; PubMed=10508784; DOI=10.1016/S0969-2126(99)80179-9;

DE FADD protein (FAS-associating death domain-containing protein)
 DE (Mediator of receptor induced toxicity).
 GN Name:FADD; Synonyms:MORT1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS.
 RC TISSUE=Umbilical vein endothelial cells;
 RX MEDLINE=95277837; PubMed=7538907; DOI=10.1016/0092-8674(95)90071-3;
 RA Chinnaiyan A.M., O'Rourke K., Tewari M., Dixit V.M.;
 RT "FADD, a novel death domain-containing protein, interacts with the
 RT death domain of Fas and initiates apoptosis.";
 RL Cell 81:505-512(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95229578; PubMed=7536190; DOI=10.1074/jbc.270.14.7795;
 RA Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,
 RA Wallach D.;
 RT "A novel protein that interacts with the death domain of Fas/APO1
 RT contains a sequence motif related to the death domain.";
 RL J. Biol. Chem. 270:7795-7798(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP INTERACTION WITH PEAL5.
 RX MEDLINE=99369240; PubMed=10442631; DOI=10.1038/sj.onc.1202831;
 RA Condorelli G., Vigliotta G., Cafieri A., Trencia A., Andalo P.,
 RA Oriente F., Miele C., Caruso M., Formisano P., Beguinot F.;
 RT "PED/PEA-15: an anti-apoptotic molecule that regulates FAS/TNFR1-
 RT induced apoptosis.";
 RL Oncogene 18:4409-4415(1999).
 RN [5]
 RP INTERACTION WITH MBD4.
 RX PubMed=12702765; DOI=10.1073/pnas.0431215100;
 RA Screaton R.A., Kieselring S., Sansom O.J., Millar C.B., Maddison K.,
 RA Bird A., Clarke A.R., Frisch S.M.;
 RT "Fas-associated death domain protein interacts with methyl-CpG binding
 RT domain protein 4: a potential link between genome surveillance and
 RT apoptosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:5211-5216(2003).
 RN [6]
 RP STRUCTURE BY NMR OF 1-83.
 RX MEDLINE=98241233; PubMed=9582077; DOI=10.1038/31972;
 RA Eberstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,
 RA Leonardo M.J., Fesik S.W.;
 RT "NMR structure and mutagenesis of the FADD (Mort1) death-effector
 RT domain.";
 RL Nature 392:941-945(1998).
 CC -!- FUNCTION: Apoptotic adaptor molecule that recruits caspase-8 or

CC caspase-10 to the activated Fas (CD95) or TNFR-1 receptors. The
 CC resulting aggregate called the death-inducing signaling complex
 CC (DISC) performs caspase-8 proteolytic activation. Active caspase-8
 CC initiates the subsequent cascade of caspases (aspartate-specific
 CC cysteine proteases) mediating apoptosis.
 CC -!- SUBUNIT: Interacts with CFLAR, PEAL5 and MBD4.
 CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues, except
 CC for peripheral blood mononuclear leukocytes.
 CC -!- DOMAIN: Contains a death domain involved in the binding of the
 CC corresponding domain within Fas receptor.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U24231; AAA86517.1; -;
 DR EMBL; X84709; CAA59197.1; -;
 DR EMBL; BC000334; AAH00334.1; -;
 DR PIR; A56912; A56912.
 DR PDB; 1AIW; NMR; @=1-91.
 DR PDB; 1AIZ; NMR; @=1-91.
 DR PDB; 1E3Y; NMR; A=89-192.
 DR PDB; 1E41; NMR; A=89-192.
 DR Genew; HGNC:3573; FADD.
 DR H-InvDB; HIX0009893; -;
 DR MiM; 602457; -;
 DR GO; GO:0005123; F:death receptor binding; TAS.
 DR GO; GO:0004871; F:signal transducer activity; IEP.
 DR GO; GO:0008625; P:induction of apoptosis via death domain rec. . ; TAS.
 DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . ; IEP.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR001875; DED.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF01335; DED; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50168; DED; 1.
 DR 3D-structure; Apoptosis.
 FT DOMAIN 3 81 DED.
 FT MUTAGEN 121 121 V->N: No interaction with Fas receptor.
 FT CONFLICT 32 32 G -> V (in Ref. 2).
 FT HELIX 3 28
 FT TURN 29 31
 FT HELIX 33 38
 FT HELIX 42 52
 FT TURN 53 53
 FT TURN 57 58
 FT HELIX 61 70
 FT TURN 71 71
 FT HELIX 73 81
 FT TURN 96 96
 FT TURN 97 106
 FT TURN 107 107
 FT HELIX 112 120
 FT TURN 123 132
 FT TURN 134 135
 FT HELIX 137 152
 FT HELIX 153 155
 FT HELIX 158 167
 FT TURN 168 169
 FT HELIX 171 185
 FT TURN 186 189
 SQ SEQUENCE 208 AA; 23279 MW; 0E65E2F852E83507 CRC64;
 Query Match 15.9%; Score 83; DB 1; Length 208;
 Best Local Similarity 27.6%; Pred. No. 7.1;

```
Matches 29; Conservative 18; Mismatches 50; Indels 8; Gaps 3;
QY 8 VHQVEEALDTDEKEMLLFLCRDVA----IDVPPNVRDLTLRERGKLSVGD---LAE 60
Db 7 LHSVSSSSLSSELTKFLGRVKRLERVQSGLDLFSNMLLEQNDLEPGHTELLRE 65
QY 61 LLYRVRFFDLKRLKMDRKAVETHLLRNPVLVSDYRVLMSEIGE 105
Db 66 LLASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDVGK 110

RESULT 25
Q6MDM0
ID Q6MDM0 PRELIMINARY; PRT; 1388 AA.
AC Q6MDM0;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Probable DNA-directed RNA polymerase, beta' chain.
GN Names=rpoc; Synonyms=tabB; OrderedLocusNames=pc0605;
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Droegge M., Frishman D.,
RA Rattai T., Mewes H.-W., Wagner M.;
RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RL the evolutionary history of chlamydiae.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAF23329.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR006592; RNA_pola_N.
DR InterPro; IPR000722; RNA_poi_A.
DR InterPro; IPR007080; RNA_poi_Rpb1_1.
DR InterPro; IPR007086; RNA_poi_Rpb1_3.
DR InterPro; IPR007083; RNA_poi_Rpb1_4.
DR InterPro; IPR007081; RNA_poi_Rpb1_5.
DR Pfam; PF04997; RNA_poi_Rpb1_1; 1.
DR Pfam; PF00623; RNA_poi_Rpb1_2; 1.
DR Pfam; PF04983; RNA_poi_Rpb1_3; 1.
DR Pfam; PF05000; RNA_poi_Rpb1_4; 1.
DR Pfam; PF04998; RNA_poi_Rpb1_5; 1.
DR SMART; SM00663; RPOLA_N; 1.
KW Complete proteome; DNA-directed RNA polymerase.
SQ SEQUENCE 1388 AA; 155296 MW; 3803E1C156B9F77D CRC64;

Query Match 15.5%; Score 81; DB 2; Length 1388;
Best Local Similarity 30.4%; Pred. No. 88;
Matches 28; Conservative 23; Mismatches 29; Indels 12; Gaps 6;
QY 1 KSRS-AEVTHOVEALDTDEK-EMLLFLCRDVAIDVPPNVRDLTLRERGKLSVGL 58
Db 208 QARKLAKRLKIETSFSSDNKEFWIMSC----VPVPPDLRPLVPL--DGRFPATSDL 261
QY 59 AELLYRV-RRFDLLKRLKMDRKAVETHLLRN 89
Db 262 NDLYRRVINRNNRLKAILKLTPTDV---IVRN 290

RESULT 26
Q68HC0
ID Q68HC0 PRELIMINARY; PRT; 247 AA.
AC Q68HC0;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Caspase 10 splice variant G.
GN Name=CASP10;
```

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pingzhang W.;
RT "Three novel isoforms of caspase family that are deficient of
RL conservative CASP domain.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY690601; AAU00989.1; -.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS50168; DED; 2.
SQ SEQUENCE 247 AA; 28363 MW; 52370B5AD12C4DCF CRC64;

Query Match 15.2%; Score 79; DB 2; Length 247;
Best Local Similarity 32.7%; Pred. No. 20;
Matches 34; Conservative 15; Mismatches 39; Indels 16; Gaps 5;
QY 12 VEEALDTDEKEMLLFLCRDVAIDVPP-----PNVRDLTLRERGKLSVGD---LAE 61
Db 27 IDSNLGVQDVENLKFLC----IGLVNKKLEKSSASDVFEHLAEDLLSEDDPPFLAEL 82
QY 62 LYRVRFFDLKRLKMDRKAVETHLLRNPVLVSDYRVLMSEIGE 105
Db 83 LYIIQKKLLQH-LNCTKEEVE-RLLPTRQRVSLFRNLLYELSE 124

RESULT 27
Q6KF63
ID Q6KF63 PRELIMINARY; PRT; 455 AA.
AC Q6KF63;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Caspase 10.
GN Name=CASP10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Vonarbourg C., Fischer A., Rieux-Laucat F.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Vonarbourg C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the peptidase C14 family.
DR EMBL; AJ487678; CAD32371.1; -.
DR HSP; P55210; 1K86.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
```

DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
KW Hydrolase; Protease; Thiol protease; Zymogen.
SQ SEQUENCE 455 AA; 51784 MW; 8E737FC3EC173616 CRC64;

Query Match 15.2%; Score 79; DB 2; Length 455;
Best Local Similarity 32.7%; Pred. No. 40;
Matches 34; Conservative 15; Mismatches 39; Indels 16; Gaps 5;

QY 12 VBEALDTDEKEMLLFLCRDVAIDVWP-----PNVRDLDDLRRGKLSVGD---LAEL 61
Db 27 IDSNLGQDVENLKFLC-----IGLVNKKLEKSSASDVFEHLAEDLLSEEDPFFLAEL 82

QY 62 LYRVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGEICE 105
Db 83 LYIIRQKKLQH-LNCTKEEVE-RLLPTRQVSLFRNLLYELSE 124

RESULT 28
Q6KF62 PRELIMINARY; PRT; 478 AA.
ID ICEA HUMAN STANDARD; PRT; 521 AA.
AC Q928E1; Q99845; Q9Y2U6; Q9Y2U7;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Caspase 10 precursor (EC 3.4.22.-) (CASP-10) (ICE-like apoptotic
DE protease 4) (Apoptotic protease Mch-4) (FAS-associated death domain
DE protein interleukin-1B-converting enzyme 2) (FLICE2).
GN Name=CASP10; Synonym=MCH4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=T-cell;
RX MEDLINE=96353838; PubMed=8755496; DOI=10.1073/pnas.93.15.7464;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=97197836; PubMed=9045686; DOI=10.1074/jbc.272.10.6578;
RA Vincenz C., Dixit V.M.;
RT "Fas-associated death domain protein interleukin-lb-converting
RT enzyme 2 (FLICE2), an ICE/Ced-3 homologue, is proximally involved in
RT CD95- and p55-mediated death signaling.";
RL J. Biol. Chem. 272:6578-6583(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C), AND VARIANT ILE-410.
RX TISSUE=Spleen, and Thymus;
RX MEDLINE=99214592; PubMed=10187817; DOI=10.1074/jbc.274.15.10301;
RA Ng P.W., Porter A.G., Janicke R.U.;
RT "Molecular cloning and characterization of two novel pro-apoptotic
RT isoforms of caspase-10.";
RL J. Biol. Chem. 274:10301-10308(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=21100893; PubMed=11161814; DOI=10.1006/geno.2000.6392;
RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.;
RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT critical region at chromosome 2q33-q34: candidate genes for ALS2.";
RL Genomics 71:200-213(2001).
RN [5]
RP PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=97121412; PubMed=8962078; DOI=10.1073/pnas.93.25.14486;
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.;
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mch5 is a Crma-inhibitable protease that activates multiple
RT Ced-3/ICE-like cysteine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
RN [6]
RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;

DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
KW Hydrolase; Protease; Thiol protease; Zymogen.
SQ SEQUENCE 455 AA; 51784 MW; 8E737FC3EC173616 CRC64;

Query Match 15.2%; Score 79; DB 2; Length 455;
Best Local Similarity 32.7%; Pred. No. 40;
Matches 34; Conservative 15; Mismatches 39; Indels 16; Gaps 5;

QY 12 VBEALDTDEKEMLLFLCRDVAIDVWP-----PNVRDLDDLRRGKLSVGD---LAEL 61
Db 27 IDSNLGQDVENLKFLC-----IGLVNKKLEKSSASDVFEHLAEDLLSEEDPFFLAEL 82

QY 62 LYRVRFDLLKRLKMDRKAVETHLLRNPHLVSDYRVLMSGEICE 105
Db 83 LYIIRQKKLQH-LNCTKEEVE-RLLPTRQVSLFRNLLYELSE 124

RESULT 28
Q6KF62 PRELIMINARY; PRT; 478 AA.
ID ICEA HUMAN STANDARD; PRT; 521 AA.
AC Q928E1; Q99845; Q9Y2U6; Q9Y2U7;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Caspase 10 precursor (EC 3.4.22.-) (CASP-10) (ICE-like apoptotic
DE protease 4) (Apoptotic protease Mch-4) (FAS-associated death domain
DE protein interleukin-1B-converting enzyme 2) (FLICE2).
GN Name=CASP10; Synonym=MCH4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=T-cell;
RX MEDLINE=96353838; PubMed=8755496; DOI=10.1073/pnas.93.15.7464;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=97197836; PubMed=9045686; DOI=10.1074/jbc.272.10.6578;
RA Vincenz C., Dixit V.M.;
RT "Fas-associated death domain protein interleukin-lb-converting
RT enzyme 2 (FLICE2), an ICE/Ced-3 homologue, is proximally involved in
RT CD95- and p55-mediated death signaling.";
RL J. Biol. Chem. 272:6578-6583(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C), AND VARIANT ILE-410.
RX TISSUE=Spleen, and Thymus;
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